

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 28, 2005, 00:24:05 ; Search time 9524 Seconds  
(without alignments)  
11081.002 Million cell updates/sec

Title: US-10-617-624-1  
Perfect score: 2178  
Sequence: 1 cctctctgttccttcctcg.....aaaaaaaaaaaaaaaaaaaaa 2178

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1617	74.2	1617	6	CQ805714	Sequence
2	1617	74.2	1617	6	AX506544	Sequence
3	1615.8	74.2	1619	8	AF056190	Arabidops
4	1614	74.1	1614	8	AF106324	Arabidops
5	1610.6	73.9	1617	8	AF685183	Arabidops
6	1610.6	73.9	1617	8	AF510074	Arabidops
7	1180	54.2	1723	8	AY189676	Brassica
8	1141.8	52.4	1641	8	AF490586	Arabidops
9	889.6	40.8	2135	8	AY028416	Citrus x
10	889.4	40.8	2485	8	AF515632	Gossypium
11	858	39.4	1752	8	AY513732	Medicago
12	858	39.4	2232	8	AY456096	Medicago
13	833.4	38.3	1656	8	AY371319	Chenopodi
14	832.8	38.2	1668	6	E63046	Na+/H+ anti
15	832.8	38.2	1668	6	E63047	Na+/H+ anti
16	832.8	38.2	2637	8	AB038492	Atriplex
17	826.4	37.9	2668	8	AY131235	Salicorni
18	821.6	37.7	1668	8	AY211397	Atriplex
19	821.2	37.7	2553	6	BD012815	Gene codi

20	821.2	37.7	2553	8	AB051818	AB051818 Nierember
21	813	37.3	2423	6	BD012814	Gene codi
22	813	37.3	2423	8	AB051817	AB051817 Petunia x
23	806.4	37.0	2263	8	AF370358	AF370358 Suaeda ma
24	805.2	37.0	2199	8	AF527625	AF527625 Tetragoni
25	786	36.1	2109	8	AY730277	AY730277 Iris lact
26	783	36.0	1623	8	AY270037	AY270037 Zea mays
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42	717	32.9	1626	8	AY270041	AY270041 Zea mays
43	696.4	32.0	2329	8	AK066444	AK066444 Oryza sat
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ALIGNMENTS

RESULT 1  
LOCUS CQ805714 1617 bp DNA linear PAT 10-MAY-2004  
DEFINITION Sequence 2125 from Patent WO2004035798.  
ACCESSION CQ805714  
VERSION CQ805714.1 GI:47111491

KEYWORDS Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE 1  
AUTHORS Inze, D., de Veylder, L. and Vlieghe, K.  
TITLE Identification of novel e2f target genes and use thereof  
JOURNAL Patent: WO 2004035798-A 2125 29-APR-2004;  
CropDesign N.V. (BE)

FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"  
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ORIGIN

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QY	286	ATGTTGGATTCTCTAGTGTGAAACTGCTTCGTTATCGACATCTGATCAGCTTCTGTG	345	
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QY	346	GTTGGTTGAATCTCTTTGTTGCACTTCTTTGTTGCTTCTTATGTTCTTGGTCATCTTTTG	405	
Db	61	GTTGGTTGAATCTCTTTGTTGCACTTCTTTGTTGCTTCTTATGTTCTTGGTCATCTTTTG	120	
QY	406	GAAGAGATAGATGATGATGAACGAATCCATCCCGCTTGTGTTGCTAGGCTAGGCACTGGT	465	
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QY	466	GTTACCATTTGTTGATTAGTAAGGAAAAAGCTGCGATCTCTCTGCTCTTTAGTGAAGAT	525	

Db 181 GTTACCAATTTTGTGATTAGTAAGAAAGAAAGCTCGCATCTTCTCGTCTTTTAGTGAAGAT 240  
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Qy 586 AAGCAGTTTTTCCGCAATTTGCTGACTATATATGCTTTTTTGGTGCTTTGGGACTATTATT 645  
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Qy 706 TTTGACTTGGGTGATATCTTCTATTTGCTGATATTTGCTGCAATTTGCTGCAATTTGCTG 765  
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Qy 826 GGTGTGTGAATGATGCAACGTCACTGTGTGCTTTCAACGGCAATTCAGAGCTTTGATCTC 885  
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Qy 1846 CCCTTTTGTTCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTTAGTAAGGCTTGA 1902  
Db 1561 CCCTTTTGTTCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTTAGTAAGGCTTGA 1617

## RESULT 2

AX506544  
LOCUS AX506544 1617 bp DNA linear PAT 27-SEP-2002  
DEFINITION Sequence 1239 from Patent WO0216655.  
ACCESSION AX506544  
VERSION AX506544.1 GI:23387781  
KEYWORDS  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana

REFERENCE 1  
AUTHORS Harper, J. P., Kreps, J., Wang, X. and Zhu, T.  
TITLE Stress-regulated genes of plants, transgenic plants containing same, and methods of use

JOURNAL Patent: WO 0216655-A 1239 28-FEB-2002;  
The Scripps Research Institute (US) ; Syngenta Participations AG (CH)  
FEATURES  
source 1. 1617  
/organism="Arabidopsis thaliana"  
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ORIGIN  
Query Match 74.2%; Score 1617; DB 6; Length 1617;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 286 ATGTTGGATTTCTTAGTGTGAAACTGCTTCGTTATCGACATCTGATCAGCTTCTGTG 345  
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RESULT 3  
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LOCUS AF056190 1619 bp mRNA linear PLN 06-JUN-2000  
DEFINITION Arabidopsis thaliana Na+/H+ exchanger (NHX1) mRNA, complete cds.  
ACCESSION AF056190  
VERSION AF056190.1 GI:6650176  
KEYWORDS  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1 (bases 1 to 1619)  
AUTHORS Quintero, F.J., Blatt, M.R. and Pardo, J.M.  
TITLE Functional conservation between yeast and plant endosomal Na(+)/H(+) antiporters  
JOURNAL FEBS Lett. 471 (2-3), 224-228 (2000)  
MEDLINE 20231718  
PUBMED 10767428  
REFERENCE 2 (bases 1 to 1619)  
AUTHORS Quintero, F.J.  
TITLE Direct Submission  
JOURNAL Submitted (30-MAR-1998) Biologia Vegetal, IRNASE (CSIC), Avda. Reina Mercedes s/n, Sevilla 41012, Spain  
FEATURES  
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Query Match 74.2%; Score 1615.8; DB 8; Length 1619;  
Best Local Similarity 99.9%; Pred. No. 0;  
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QY 1244 TGGATGCTTGGACATTTGCAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCG 1303  
DB |||||  
961 TGGATGCTTGGACATTTGCAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCG 1020  
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DB |||||  
1021 CAGTGAGCTCAATCTCTAATGGGTCTGGTCAATGGTTTGGAGAGCAGCGTTTCGTCTTCGGT 1080  
QY 1364 TATCGTTCTTATCTTAACCTTAGCCAGAGAAATCAAGCGAGAAATCACTTTTAACATGC 1423  
DB |||||  
1081 TATCGTTCTTATCTTAACCTTAGCCAGAGAAATCAAGCGAGAAATCACTTTTAACATGC 1140  
QY 1424 AGGTTGTGATTTGGTGGTCTGCTCATGAGAGGTGCTGTATCTATGCTTATGCTATCA 1483

DB 1141 AGGTTGTGATTTGGTGGTCTGCTCATGAGAGTGTGTATCTATGCTTGTGATACA 1200  
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QY 1844 TACCTTTTGTTCAGGTTCTCCAACTGAGAGAAACCCCTCTGTATCTTGTAGAGCTTGA 1902  
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RESULT 4  
AF106324  
LOCUS 1614 bp mRNA linear PLN 03-MAR-1999  
DEFINITION Arabidopsis thaliana sodium proton exchanger Nhx1 mRNA, partial cds.  
ACCESSION AF106324  
VERSION AF106324.1 GI:4324596  
KEYWORDS Arabidopsis thaliana (thale cress)  
SOURCE Arabidopsis thaliana  
ORGANISM Arabidopsis thaliana  
REFERENCE 1 (bases 1 to 1614)  
AUTHORS Gaxiola,R.A., Rao,R., Sherman,A., Grisafi,P., Alper,S.L. and Fink,G.R.  
TITLE The Arabidopsis thaliana proton transporters, AtNhx1 and Avp1, can function in cation detoxification in yeast  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (4), 1480-1485 (1999)  
MEDLINE 99145575  
PUBMED 9990049  
REFERENCE 2 (bases 1 to 1614)  
AUTHORS Gaxiola,R.A., Rao,R., Sherman,A., Grisafi,P., Alper,S.L. and Fink,G.R.  
TITLE Direct Submission  
JOURNAL Submitted (12-NOV-1998) Whitehead, Nine Cambridge Center, Cambridge, MA 02142, USA  
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## ORIGIN

Query Match		74.1%; Score 1614; DB 8; Length 1614;
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DB	1	ATGTTGGATCTCTAGTGTGCGAACTGCTTCGTTATCGACATCTGATCACGCTTCTGTG 60
QY	346	GTTCGGTGAATCTCTTTCGACCTCTTTCGCTTGTATGTTCTTGGTCACTTTTG 405
DB	61	GTTCGGTGAATCTCTTTCGACCTCTTTCGCTTGTATGTTCTTGGTCACTTTTG 120
QY	406	GAAGAGATAGATGATGAACCAATCCATCACCGCTTCTGATTGGGCTAGGCACTGCT 465
DB	121	GAAGAGATAGATGATGAACCAATCCATCACCGCTTCTGATTGGGCTAGGCACTGCT 180
QY	466	GTACCATTTTGTGATTAGTAAAGGAAAGCTCGCATCTTCTCGTCTTTAGTGAAGAT 525
DB	181	GTACCATTTTGTGATTAGTAAAGGAAAGCTCGCATCTTCTCGTCTTTAGTGAAGAT 240
QY	526	CTTTTCTTCATATATCTTTTGGCCACCATATATTAATGACAGGTTTCAAGTAAAG 585
DB	241	CTTTTCTTCATATATCTTTTGGCCACCATATATTAATGACAGGTTTCAAGTAAAG 300
QY	586	AAGCAGTTTTCGCAATTCGTGACTATATGCTTTTTTGGTGTGTTGGGACTATTAT 645
DB	301	AAGCAGTTTTCGCAATTCGTGACTATATGCTTTTTTGGTGTGTTGGGACTATTAT 360
QY	646	TCTTGACAAATCATATCTCTAGGTGTAAACAGTTCTTTTAAAGAGTTGGACATTTGA 705
DB	361	TCTTGACAAATCATATCTCTAGGTGTAAACAGTTCTTTTAAAGAGTTGGACATTTGA 420
QY	706	TTTGACTGGGTGATATCTTCTATGTGTCATATTTGCTGCAACAGATTCAGTATGT 765
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QY	766	ACACTGCAGTTCTGAATCAAGCAGACACCTTTGCTTTACAGTCTTGTATTCGAGAG 825
DB	481	ACACTGCAGTTCTGAATCAAGCAGACACCTTTGCTTTACAGTCTTGTATTCGAGAG 540
QY	826	GGTGTGTGAATGATGCAACGTGAGTTGTGTCCTTCAACGCGATTCAGAGCTTTGATCTC 885
DB	541	GGTGTGTGAATGATGCAACGTGAGTTGTGTCCTTCAACGCGATTCAGAGCTTTGATCTC 600
QY	886	ACTCACCTAAACACAGAGCTGCTTTTCACTTCTTTGGAACCTCTTGTATTTGTTCTC 945
DB	601	ACTCACCTAAACACAGAGCTGCTTTTCACTTCTTTGGAACCTCTTGTATTTGTTCTC 660
QY	946	CTAAGTACCTCTGCTGCTGCAACCGGTCTGATAGTGCATGCTTATGCTTATGCGTATCTT 1005
DB	661	CTAAGTACCTCTGCTGCTGCAACCGGTCTGATAGTGCATGCTTATGCTTATGCGTATCTT 720
QY	1006	TACTTTGGAAGCACTCAACTGACGAGAGGTGCGCTTATGATGCTTATGCGTATCTT 1065
DB	721	TACTTTGGAAGCACTCAACTGACGAGAGGTGCGCTTATGATGCTTATGCGTATCTT 780
QY	1066	TCTTATATGCTTGTGAGCTTTTCGACTTGTAGCGGTATCTCACTGTGTTTCTGTGCT 1125
DB	781	TCTTATATGCTTGTGAGCTTTTCGACTTGTAGCGGTATCTCACTGTGTTTCTGTGCT 840
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DB	841	ATTGTGATGCTCCATTCACATGCGACATGTAAACGAGAGCTCAAGATTAACACAAAG 900

QY	1186	CATACCTTTGCAACTTTTGTCTATTTCTTCGCGAGACATTTATTTTCTTGTATGTTGGAATG 1245
DB	901	CATACCTTTGCAACTTTTGTCTATTTCTTCGCGAGACATTTATTTTCTTGTATGTTGGAATG 960
QY	1246	GATGCTTTGGACANTTGAACAAGTGGAGATCCGTGAGTGACACACCGGGAAACATCGATCGCA 1305
DB	961	GATGCTTTGGACANTTGAACAAGTGGAGATCCGTGAGTGACACACCGGGAAACATCGATCGCA 1020
QY	1306	GTGAGCTCAATCTTAATGGGTCTGCTCATGTTTGAAGAGCAGCGTTCGTCTTTCCGTTA 1365
DB	1021	GTGAGCTCAATCTTAATGGGTCTGCTCATGTTTGAAGAGCAGCGTTCGTCTTTCCGTTA 1080
QY	1366	TGCTTTCTATCTAATCTAGCCAAAGAAATCAAAGCGAGAAATCAACTTTTAAATGACAG 1425
DB	1081	TGCTTTCTATCTAATCTAGCCAAAGAAATCAAAGCGAGAAATCAACTTTTAAATGACAG 1140
QY	1426	GTTCGTGATTTGGTGGTCTGCTCATGAGAGGTGCTGTATCTATGGCTCTTGCATACAC 1485
DB	1141	GTTCGTGATTTGGTGGTCTGCTCATGAGAGGTGCTGTATCTATGGCTCTTGCATACAC 1200
QY	1486	AAGTTTACAAGGCGCGGCACACAGATGTACGCGGAAATGCAATCATGATCACGATGACG 1545
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QY	1546	ATAACTGTCTGTCTTTTATAGCACAGTGTGTTGATGTCGACCAACCACTCTATAAGC 1605
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QY	1606	TACCTATTACCGCACAGAACCGCACACAGCATGTTATCTGATGACACACACCCCAAAA 1665
DB	1321	TACCTATTACCGCACAGAACCGCACACAGCATGTTATCTGATGACACACACCCCAAAA 1380
QY	1666	TCCATACATATCCCTTTGTTGACCAAGACTCGTTTCATTGAGCCCTTCAGGGAACCAACAAT 1725
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QY	1726	GTGCTCGGCTGACAGTATACGTGGCTTTTGACACGCGCCACTTCGAACCGTGCATTAC 1785
DB	1441	GTGCTCGGCTGACAGTATACGTGGCTTTTGACACGCGCCACTTCGAACCGTGCATTAC 1500
QY	1786	TACTGGAGACAAATTTGATGACTCTTTCATGCGACCGCTCTTTGGAGGTCTGGCTTTGTA 1845
DB	1501	TACTGGAGACAAATTTGATGACTCTTTCATGCGACCGCTCTTTGGAGGTCTGGCTTTGTA 1560
QY	1846	CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTAGTAAGGCT 1899
DB	1561	CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTAGTAAGGCT 1614
RESULT 5		
AY685183		1617 bp mRNA linear PLN 16-AUG-2004
LOCUS		Arabidopsis thaliana sodium proton exchanger (NHX1) mRNA, complete cds.
DEFINITION		Arabidopsis thaliana (thale cress)
ACCESSION		AY685183
VERSION		AY685183.1 GI:51094439
KEYWORDS		Arabidopsis thaliana
SOURCE		Arabidopsis thaliana
ORGANISM		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE		1 (bases 1 to 1617)
AUTHORS		Wang, D., Zhang, J.L. and Zhang, J.W.
TITLE		Direct Submission
JOURNAL		Submitted (14-JUL-2004) Agronomy College, Institute of Agrobiotechnology, Labzhou, Gansu 730070, China
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RESULT 7
AY189676
LOCUS      AY189676               1723 bp      mRNA      linear      PLN 20-NOV-2003
DEFINITION Brassica napus Na+/H+ vacuolar antiporter mRNA, complete cds.
ACCESSION  AY189676
VERSION     AY189676.1   GI:37778921
KEYWORDS
SOURCE      Brassica napus (rape)
ORGANISM    Brassica napus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 1723)
            Wang, J., Zuo, K.-J., Wu, W.-S., Song, J., Sun, X.-F., Lin, J., Li, X.-F.
            and Tang, K.-X.
            Molecular cloning and characterization of a new Na+/H+ antiporter
            gene from Brassica napus
            DNA Seq. 14 (5): 351-358 (2003)
REFERENCE   2  (bases 1 to 1723)
            Wang, J., Zuo, K.-J., Wu, W.-S., Sun, X.-F., Li, X.-F. and Tang, K.-X.
            Direct Submission
            Submitted (30-NOV-2002) Institute of Genetics, Life Sciences, Fudan
            University, Handan 220, Shanghai 200433, China
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Query Match      54.2%; Score 1180; DB 8; Length 1723;
Best Local Similarity 86.7%; Pred. No. 4.4e-253;
Matches 1339; Conservative 0; Mismatches 190; Indels 15; Gaps 3;

Qy  280  ATAACAATGTTGGATCTCTAGTCGCAAACTGCCTTCGTTATCGACATCTGATCAGCCT 339
Db  163  AAAACAATGTTGGATCTCTAGTCGCAAACTGCCTTCGTTATCGACATCTGATCAGCCT 222

Qy  340  TCTGTGGTTCGGTGAATCTCTTTGTTGCACTTCTTTGTTGCTTGTGATTTGTTCTTGGTCA 399
Db  223  TCTGTGGTTCGGTGAATCTCTTTGTTGCACTTCTTTGTTGCTTGTGATTTGTTCTTGGTCA 282

Qy  400  CTTTGTGGAAGAGATAGATGATGAACCAATCCATCCAGCGCTTGTGATTTGGGCTAGGC 459
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Qy  460  ACTGTGTTTACCATTCTTGTGATTAAGAGAAAAAGCTCGCATCTTCTCGTCTTTAGT 519
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Qy  520  GAAGATCTTTCTTCATATATCTTTTGGCCACCATTATATTCAATGCGAGGTTTCAAGTA 579
Db  403  GAAGATCTTTCTTCATATATCTTTTGGCCACCATTATATTCAATGCGAGGTTTCAAGTA 462

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Qy  580  AAAAAGAAGCAGTTTTTTCGCAATTTTCGTGACTATTATATGCTTTTGGTGTCTTGGGACT 639
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Qy  640  ATTATTTTTCGCAATCATATCTCTAGGTGTAAACACAGTTCTTTTAAAGAAGTTGGACATT 699
Db  523  GTTGTCTCTTGCACCTGTCATAACTCTAGGTGTAAACACAGTTCTTTTCAAGAAATCGACATT 582

Qy  700  GGAACCTTTGACCTGGGTGATTAATCTTGCTATTGGTGCCATATTTGCTGCAACAGATTCA 759
Db  583  GGGACCTTTGACCTGGGTGATTAATCTTGCAATTTGGTGCATATTTGGCGCAACAGATTCT 642

Qy  760  GTATGTACACTGCAGGTTCTGAATCAAGACGACACCTTTGCTTTTACAGTCTTGTATTTC 819
Db  643  GTGTGCACACTGCAGGTTCTGAATCAAGATGAGACACCTTTGCTTTTACAGTCTTGTATTTC 702

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Db  703  GGAGAAGTTGTGTGAATGATGCCACATCAGTTGTGTGCTTTCACAGCCATTCAGAGCTTT 762

Qy  880  GATCTCACTCACTAAACACGAGCTGCTTTTTCATCTCTTGGAAAACCTTCTTGTATTG 939
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Qy  940  TTTCTCTTAAGTACCTTGTGCTGCTGCAACCGGCTCTGATAAGTGCATGTTATCAAG 999
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Qy  1000  AAGCTATACCTTTGGAAGGCACTCAACTGACCG --- AGAGGTTGCTTATGATGCTTATG 1056
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Qy  1057  GCGTATCTTCTTATATGCTTGTGAGCTTTTTCAGCTTGTGAGCGGTATCTCCTACGTGTGTT 1116
Db  943  GCATATCTTCTTATACATGCTTGTGAGCTATTTCCCTTGTGAGTGTGTTTCTCCTGTGTTTC 1002

Qy  1117  TTCTGTGCTATGATGATGCCATTACACATGCGCACAAATGTAAACGGAGAGCTCAAGAATA 1176
Db  1003  TTCTGTGCTATGATGATGCCATTACACATGCGCACAAATGTAAACGGAGAGCTCAAGAGTA 1082

Qy  1177  ACAACAAAGCATACCTTTTGCAACTTTGTCTCACTTTCTTGGGAGACATTTATTTCTTGAT 1236
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Qy  1237  GTTGAATGATGCTCTGGACATTTGACAAAGTGGAGATCCGTGAGTGACACACCCGGGACA 1296
Db  1123  GTCGGGATGATGATGATGAGCATCGAGAAGTGGAGATTCGTGAGTGCAGCCCGGGGACA 1182

Qy  1297  TCGATCGCAGTGAAGCTCAATCCTTAATGGGTCTGCTCATGTTTGAAGAGCAGCGTTCGTC 1356
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Qy  1357  TTTCCGTTATCGTTTCTATCTTAACCTAGCCAAGAAGAAATCAAAGCGAGAAATAACAACCTT 1416
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Qy  1477  GCATACAAACAAGTTTACAAGGGCGGGCACACAGATGTACGCGGAATGCAATCATGATC 1536
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Qy  1537  ACGAGTACGATAACTGTCTGTCTTTTGTAGCAGAGTGGTGTGTTGGTATGCTGACCAACCA 1596
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Qy  1657  ACCCAAAATCCATACATATCCCTTTGTT-----GGACCAAGACTCGTTTCATTGAG 1707

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Qy	1540	AGTACGATAACT	GTCTGCTCTTTT	TAGACACAGTGTG	TGTTGCTATGCT	GACCAACCACTC		1599
Db	1261	AGTACAATACCG	TCTGTCTTTT	TAGCACCATGTGT	TGGTAGCTGT	TAAACCAACCACTG		1320
Qy	1600	ATAAGCTACCTT	ATPACCGCACCGA	ACGC-----	CACCACGAGCATG	TGTTATCTGAT		1650
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Qy	1702	ATTGAGCGCTTC	CAGGGAACCAAT	TGTCCTCGGCGCT	GACAGTATACG	TGTGCTTCTTTGACA		1761
Db	1441	GAGTTACCTGG	GAGCCACGAGG	AGTGCACGACCA	ACAGCCTTCGAGG	TTTTCTCTCATG		1500
Qy	1762	CGGCCCACTCG	AACCGTGCAATT	ACTGAGAGACA	AAATTGATGACT	CCTTCATCGGACCC		1821
Db	1501	CGCCCCACCG	AGCTGTCCACTA	TTACTGAGACAG	TTTGATGCTCTT	CATCGCGTCT		1560
Qy	1822	GTCTTTGGAGT	CGTGTGCTTTG	TACCTTTGTTTCC	AGGTTCTCCA	CTGAGAGAAACCT		1881
Db	1561	GTGTTTGGTGT	CGCGAATTCGT	TCCCTTTGTCCCTG	GTTCCTGCTG	CTCGAGTGAAGAGCAGC		1620
Qy	1882	CCTGATCTT	AGTAGGCTTGA					1902
Db	1621	CATGATCTT	AGTAAACCTTGA					1641

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RESULT 9
AY028416 LOCUS
DEFINITION Citrus x paradisi sodium/proton exchanger mRNA, complete cds.
ACCESSION AY028416
VERSION AY028416.2 GI:15812034
KEYWORDS Citrus x paradisi
SOURCE Citrus x paradisi
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Sapindales; Rutaceae; Citrus.
1 (bases 1 to 2135)
Porat,R., Povancello,D., Ben-Hayyim,G. and Lurie,S.
A heat treatment induced the expression of a Na+/H+ antiport gene
(GNHX1) in citrus fruit
JOURNAL Plant Sci. 162 (6), 957-963 (2002)
REFERENCE 2 (bases 1 to 600)
AUTHORS Porat,R., Lurie,S. and Povancello,D.
TITLE Direct Submission
JOURNAL Submitted (05-MAR-2001) Postharvest Sciences, ARO, The Volcani
Center, Bet Dagan 50250, Israel
3 (bases 1 to 2135)
Porat,R., Lurie,S. and Povancello,D.
Direct Submission
JOURNAL Submitted (01-OCT-2001) Postharvest Sciences, ARO, The Volcani
Center, Bet Dagan 50250, Israel
REMARK Sequence update by submitter
COMMENT On Oct 1, 2001 this sequence version replaced gi:13508486.
FEATURES
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132..1760
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CDS

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1886 AGACCAATCCATCCCAAAATCAATGGAGGACCAATTTCTCGAAGCGGCCAGGACTCTTT 1945  
1707 GCTTTTCAGGAACCAATATGTCCTCGGCTGACAGATATAGTGGCTTTCTTGACACGCCC 1766  
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QY 1827 TGGAGGTGCGTGGCTTTGTAACCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCTCTCTGA 1886  
Db 2066 TGGTGGCGGGTTTTGTGCGCTTCGTTCTGCTGCTCCCAACAGAAAGGAGTGAACCTAA 2125  
QY 1887 TCTTAGTAAGCTTTGAGGCTAACTGGAAGAAAAGCTTTT 1925  
Db 2126 TCTGCTCAATGGCAATGAGGTGTTGAAACAAGATCTCT 2164

RESULT 11  
AY513732  
LOCUS  
DEFINITION  
Medicago sativa Na+/H+ antiporter mRNA, complete cds.  
ACCESSION  
AY513732  
VERSION  
AY513732.1 GI:46250920  
KEYWORDS  
SOURCE  
ORGANISM  
Medicago sativa  
Medicago sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.  
REFERENCE  
1 (bases 1 to 1752)  
An,B.Y. and Zhang,X.S.  
TITLE  
Isolation and expression of MeNHX1 gene in alfalfa  
JOURNAL  
Unpublished  
REFERENCE  
2 (bases 1 to 1752)  
An,B.Y. and Zhang,X.S.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (27-DEC-2003) College of Life Sciences, Shandong  
Agricultural University, Daizong Street, Taian, Shandong 271018,  
P.R. China  
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CDS  
39,48; Score 858; DB 8; Length 1752;  
Best Local Similarity 72.08; Pred. No. 4.2e-181;  
Matches 1148; Conservative 0; Mismatches 440; Indels 6; Gaps 2;

ORIGIN  
Query Match 39,48; Score 858; DB 8; Length 1752;  
Best Local Similarity 72.08; Pred. No. 4.2e-181;  
Matches 1148; Conservative 0; Mismatches 440; Indels 6; Gaps 2;

QY 290 TGGATTTCTAGTGTGAAACTGCTTCGTTATCGACATCTGATCAGCTTCTGTGGTTG 349  
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Db 200 CTATGAACCTTTGTTGTGGCACTTCTGTGCTGTGTTATTTGTTGTTGTTCTCGAGG 259  
QY 410 AGAATAGATGATGAACGAATCCATCCCGCTTTGTTGATTGGGCTAGGCACTGGTGTTA 469

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## RESULT 12

AY456096 LOCUS 2232 bp mRNA linear PLN 23-NOV-2003  
DEFINITION Medicago sativa Na+/H+ antiporter mRNA, complete cds.  
ACCESSION AY456096  
VERSION AY456096.1 GI:38373524

## SOURCE

Medicago sativa  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.

## REFERENCE

1 (bases 1 to 2232)  
Yang, Q.C., Wu, M.S. and Wang, P.Q.  
The gene encoding Na+/H+ antiporter cloned from alfalfa  
Unpublished  
2 (bases 1 to 2232)  
Yang, Q.C., Wu, M.S. and Wang, P.Q.  
Direct Submission  
Submitted (01-NOV-2003) Turf & Forage Science, Chinese Academy of  
Agricultural Science (CAAS), No.2 Yuanmingyuan West Road, Haidin,  
Beijing 100094, China

## FEATURES

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## ORIGIN

Query Match		39.4%;	Score 858;	DB 8;	Length 2232;
Best Local Similarity		72.0%;	Pred. No. 4,1e-181;		
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DB	349	TGCTCTCTATTGTTTCAAAATCATCAATGTTATCCACATCCGATCATGCTTCTGTGTTT	408		
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DB	409	CTATGAACCTTGTGTTGGACATCTCTGTGCTGTGTTATTTGCTGTTGCTCATCTTCTCGAGG	468		
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DB	529	TGATTTTGTCTGTTAGTGGTGAAGAAAGTTCGCAATATTTCTTGTTCAGTGAAGATCTTT	588		
QY	530	TCTTCATATATCTTTTGGCACCCATTAATTCATGAGGGTTTCAAGTAAAAAGAAAGC	589		
DB	589	TCCTTATATACCTTCTGCGGCTATTATATTCATATGCGGGTTTCAAGTAAAGAAAGC	648		
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QY	650	GCACAATCATATCTCTAGGTGTAACACAGTTCTTTAAGAAGTTGGACATTTGGAACCTTTG	709		
DB	709	GTGTCATTAATACACAGGGTCTACTTTTGTCTTTTAAAGGATGGATATTGGGCCACTGG	768		
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QY	770	TGCAGTTTCTGAATCAACAGCAGACACCTTTGCTTTACAGTCTTGTTTTCGGAGGGTG	829		
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QY	830	TTGTGAATGATGACACAGTCAAGTTGTGCTTTCAACGCAATTCAGAGCTTTGATCTCACTC	889		
DB	889	TTGTGAATGATGATCACTCAGTGTGCTTTTCAATGCAATTCAGAGCTTTGATCTTAACC	948		
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QY	950	GTACCTTCTGCTGCTGCAACCGTCTGATAAGTGGTATGTTATCAAGAGCTATACT	1009		
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DB	1189	TTATGCTCATTAATCTGGCATATGTCGCGAGGTTCAGATCACTACCAAGCANT	1248		
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Db	1369	GTTCAGTATTGTTGGGCTAATACTTCTTGGAAAGACAGCGTTTGTGTTTTCCCTTATCCT		1428
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Qy	1430	TGATTTGGTGTCTTGGTCTCATGAGAGGTGCTGTATCTATGGCTCTTTCGATACAAACAAGT		1489
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DEFINITION	Chenopodium glaucum Na+/H+ antiporter (NHX) mRNA, complete cds.				
ACCESSION	AY371319				
VERSION	AY371319.1				
KEYWORDS	GI:34484303				
SOURCE	mitochondrion Chenopodium glaucum				
ORGANISM	Chenopodium glaucum				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Chenopodium.				
AUTHORS	1 (bases 1 to 1656)				
TITLE	Li, J., Zhang, F., Ma, J., Cai, L. and Wang, Y.				
JOURNAL	Using RT-PCR to Amplify the NHX Gene Fragment in Chenopodium glaucum				
REFERENCE	2 (bases 1 to 1656)				
AUTHORS	Zhang, F., Li, J., Ma, J., Cai, L. and Wang, Y.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-AUG-2003) College of Life Science and Technology, Xinjiang University, 14 Shengli Road, Urumqi, Xinjiang 830046, China				
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## ORIGIN

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 Best Local Similarity 71.4%; Pred. No. 1.3e-175;  
 Matches 1136; Conservative 0; Mismatches 431; Indels 24; Gaps 2;

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 VERSION E63046.1 GI:18628471  
 KEYWORDS JP 2000157287-A/1.  
 SOURCE unidentified  
 ORGANISM unclassified.  
 REFERENCE 1 (bases 1 to 1668)  
 AUTHORS Shono, M., Hayakawa, T. and Tanaka, A.  
 TITLE Na+/H+ antiporter protein and gene encoding it  
 JOURNAL Patent: JP 2000157287-A 1 13-JUN-2000;  
 COMMENT PLANTECH RESEARCH INSTITUTE  
 OS Atlliplex gmelini



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PC C12N15/09, A01H5/00, C07K14/415, C12Q1/68//C12N5/10, C12N15/00, PC
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QY 323 CGACATCTGATCACGCTTCTGTGTGCGTTCGAATCTCTTTTTCGACTCTTTTGTGCTT 382
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TITLE Na+/H+ antiporter protein and gene encoding it
JOURNAL Patent: JP 200157287-A 2 13-JUN-2000;
PLANTECH RESEARCH INSTITUTE
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5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsa1:\*  
9: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	671.6	30.8	2080	3	AY105332 Zea mays
2	630.6	29.0	3272	3	AY109416 Zea mays
3	595.6	27.3	651	6	C99909 C99909 Arab
4	487.2	22.4	834	6	CA767092 AF53-Rpt
5	478.8	22.0	1449	9	CL973674 OsIFCC024
6	435.8	20.0	483	5	BP570332 BP570332
7	432.8	19.9	966	7	CK360919 EST706997
8	432	19.8	433	1	AV792419 AV792419
9	429.4	19.7	629	1	AV825792 AV825792
10	422.4	19.4	448	6	CD531888 12G22 Ara
11	416.6	19.1	733	5	BU004460 QGGE06.Y
12	416.2	19.1	827	7	CO094724 GR_Ea17A
13	415.8	19.1	1212	2	BE420587 HMM000.D1
14	415	19.1	827	7	CO085721 GR_Ea03A
15	414.2	19.0	852	6	CB681657 OSJNEf08D
16	412.4	18.9	767	7	CF479378 RTW323
17	411	18.9	743	6	CA484823 WHE4311.B
18	409.6	18.8	690	5	BQ865196 QGC2a03.Y
19	408	18.7	420	1	AV788758 AV788758
20	406.2	18.7	719	4	BJ312595 BJ312595
21	401.4	18.4	804	7	CO100982 GR_Eb002
22	400.8	18.4	615	5	BQ589958 S015138-0
23	397.8	18.3	404	5	BP609318 BP609318
24	396.4	18.2	665	4	BI933988 EST553877

25	396.2	18.2	786	7	CF208932
26	396	18.2	719	5	BU039126 PP_LRa000
27	385	17.7	658	7	CO099045 GR_Ea23L
28	381.2	17.5	420	5	BP565077 BP565077
29	380.4	17.5	772	6	CD486155 CFUS6.4D1
30	375.4	17.2	830	7	CK862028 33159 In
31	375.2	17.2	619	5	BU926933 sas93e08.
32	373	17.1	589	7	CN909560 030123ABL
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34	370	17.0	833	6	CB668797 OSJNEd16N
35	365.8	16.8	369	1	AV815619 AV815619
36	359.6	16.5	736	6	CA238161 SCEQPL505
37	351.4	16.1	761	6	CA197063 SCBFAD109
38	350.8	16.1	756	6	CA243274 SCBGLP109
39	350.6	16.1	607	5	BQ612167 sap8d01.
40	349.8	16.1	802	5	BQ512490 EST619905
41	346.8	15.9	709	7	CO528231 3530_1.18
42	345.6	15.9	664	6	CA246092 SCEZFL508
43	345	15.8	666	6	CA216351 SCRLFL402
44	343.8	15.8	542	7	CN890706 010513AAx
45	343.4	15.8	706	4	BJ291707 BJ291707

ALIGNMENTS

RESULT 1  
AY105332 2080 bp mRNA linear HTC 16-OCT-2002  
LOCUS AY105332 Zea mays PC0131050 mRNA sequence.  
DEFINITION Zea mays  
ACCESSION AY105332  
VERSION AY105332.1 GI:21208410  
KEYWORDS HTC.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 2080)  
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitesitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.  
TITLE Zea Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes  
JOURNAL Unpublished (2002)  
REFERENCE 2 (bases 1 to 2080)  
AUTHORS Coe,E.H.  
TITLE Direct Submission  
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA  
COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES

Location/Qualifiers  
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/note="this sequence is part of a project of EST assemblies resulting from the application of public configs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match 30.8%; Score 671.6; DB 3; Length 2080;

Best Local Similarity 65.5%; Pred. No. 7.4e-149; Matches 1029; Conservative 0; Mismatches 534; Indels 7; Gaps 3;			
Qy	318	GTATATCGACATCTCATCAGCGTCTCTGTGGTTGTGAATCTCTTTTGTTCGACATCTTTG 377	
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Qy	378	TGCTTGTATTGTTCTTGCTCATCTTTTGGAGAGAAATAGATGGATGAACGAATCCATCAC 437	
Db	285	CAGCTGATTTGTCATCGGCCACTTGTCTGGAAGGNAACGATGGGTGAACGAGTCCATCAC 344	
Qy	438	CGCCTTGTGATTTGGCTAGGCACTGGTGTTAACATTTTGTGATTAAGTAAAGAAAGAAG 497	
Db	345	CGCGCTTGTATGGGCTCATCAACGGAGGCGTCATCTGCTGCTTACTAATATGGACAAA 404	
Qy	498	CTCGCATCTCTCTGCTCTTTAGTGAAGATCTTTTCTCATATATCTTTTGCACCCATTAT 557	
Db	405	CTCAGCATTTCTTGTTTTCAGCGAGGACCTGTTTTCATATATTTTACTTCGCCGATTAAT 464	
Qy	558	ATTCAATGCGAGGGTTTCAAGTAAAAAAGAACGAGTTTTTCGCGAATTTTCGTGACTATTAT 617	
Db	465	CTTCAATGCCGGTTTCAAGTAAAGAAAGCAATTTCTTCGCAACTTTTAAACGATTAAT 524	
Qy	618	GCTTTTGGTGTCTTGGGACTATTATTTCTTGCACAATCATATCTCTAGGTGTAAACACA 677	
Db	525	TTTGTTTGGTGTATTGGGACTCTGATTTCTTTTGTAAATAATCTCTCTTGGTGTATGGG 584	
Qy	678	GTTCTTTAAAGAGTTTGACATTGGAACCTTTTGACTTGGGTGATTTATCTTGTCTATTGGTGC 737	
Db	585	GTTGTTCAAGAAACTTGATTTGGTGCACCTCGAGCTTGGGAGCTATCTTTGCAATTTGGTGC 644	
Qy	738	CATATTTGCTGCAACAGATTCAAGTATGTACACTCGAGTTCTGAATCAAGACAGACACACC 797	
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Qy	798	TTTGCTTTACAGTCTTGATTTCCGAGAGGGTTGTGAATGATGCAACAGTCAGTTTGGT 857	
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Qy	858	CTTCAACGCGATTCAGAGCTTTGATCTCACTCACTTAACCAAGAGCTGCTTTTCATCT 917	
Db	765	CTTCAATGCAATTGAACACCTTGATATGTAATTTTGTGATGCTATTTGTTGTAATTT 824	
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Db	825	CGTCGGAAATTTCTCTACTTGTCTTCAACGACACCATCTTGAGTAGTACCGGGTT 884	
Qy	978	GATAAGTCCGTATGTTATCAAGAAAGCTATACTTTTGGAGGCACTCAACTGACCGAGAGGT 1037	
Db	885	GCTTAGTGTCATACATTAACAAGAGCTCTGTTTGGCCAGACATTTCACTGATAGAGAAGT 944	
Qy	1038	TGCCCTTATGATGCTTATGGGATCTTTTCTTATATGCTTGCTGAGCTTTTCGACTTTGAG 1097	
Db	945	TTCTATCATGATCTCATGGCATACCTTTTCAATACATGATATCAATGCTGTTGGACCTGAG 1004	
Qy	1098	CGGTATCTCACTGCTGTTTTTCTGTGTTATTGTGATGTCCCATTTACATATGCGCAATATG 1157	
Db	1005	TGGAAATTTCTACTGTTCTTCTGTGGAAATAGTAATGTCACTTTACACTTTGGCATATATG 1064	
Qy	1158	AACGGAGAGCTCAAGAATAACAACAAAGCATACCTTTTGCAACTTTGTCAATTTCTTGGCGA 1217	
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Qy	1218	GACATTTATTTTCTTGATGTGTGAATGGATGCCCTTGACATTTGACAAGTGGAGATCCGT 1277	
Db	1125	AAATTTTCTCTCTCTATGTTGGATGGATGCAATGACATTTGGAAGTGGAAATTTAGC 1184	
Qy	1278	GAGTGACACACCGGGAACATCGATGCG - AGTGAGCTCAATCTTAATGGGTCTGTGTCATGG 1336	
Db	1185	TAGTAGCAGTCTTAAGAAACCAATTCGTTTAAAGTGCAATTTATTTTGGGCTTGGTTATGG 1244	
Qy	1337	TTGGAAGACGACGCTTCGTCTTTCCGTTATCGTTTCTATCTTAACCTTAGCCAAAGAAATC 1396	

Query Match	29.0%;	Score 630.6;	DB 3;	Length 3272;
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Matches 1061;	Conservative 0;	Mismatches 674;	Indels 16;	Gaps 4;
Qy	265	TGGATCTAGAGAGATACAAATGTTGGATTCTCTAGTGTGCGAATCGCCTTCGTTATCG	324	
Db	22	TGACTGTGAGGGCAGATGGGCTNNNNCTCGATGGCGCTGGCGCTGGGCGACCCG	81	
Qy	325	ACATCTGATCACGCTTCTGTGGTTGGCTTGAATCTCTTTGTGTGACATCTCTTTGTGCTTGT	384	
Db	82	CCAGCGACTACGCTCCATCGCGCGGTGGGCTGTNNNNNNNNNNNNNNNNNNNNNN	141	
Qy	385	ATTGTTCTTGGTCACTTTTGGAAAGAAATAGATGGATGAACGAATCCATCACCGCCCTTG	444	
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Qy	445	TTGATTGGGCTAGCACGTGTGTACCATTTTGTGTGATTAGTAAGAGAAAGCTCCGAT	504	
Db	202	TTCATCGGGCTGGAACTGGAGCGGTCACTCCTGTTCCGCTCGACGGGAAAGCATTCGCGC	261	
Qy	505	CTTCTCGCTTTAGTGAAGATCTTTTCTTCATATATCTTTTGGCCACCATTATATATCAAT	564	
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Qy	625	GGTGCTTTGGGACTATTATTTCTTGACAAATCATATCTCTAGGTGTAAACAGTTCCTT	684	
Db	382	GGTGCACTTGGCACCTTGATCTCTTTTACTGTGTAATATCCCTTGGCGCTCTAGGACTAATA	441	
Qy	685	AAGAAGTTGGACATTTGGAACTTTGACTTGGGTGAATTATCTTGCTATTGGTGCCATATTT	744	
Db	442	TCAAGGCTTAATATCGCGGCNCTTGAATCGGAGACATATCTTGCACTTGGGCAATATC	501	
Qy	745	GCTGCAACAGATTCAGTATGTACACTGCAGGTTCTGAATCAAGACGAGACACCTTTGCTT	804	
Db	502	TCGSCCAGACTCGGTTTGACCTTGCAGGTGTAAAGCCAAGATGAGACACCATCTTG	561	
Qy	805	TACAGTCTTGTAATTCGAGAGAGGTGTGTGNAATGATGCAACGTCAGTTGTGTTCTTCAAC	864	
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Qy	865	GCGATTTCAGAGCTTTGATCTCACTCACTAAACCAACGAAGCTGCTTTCTCTCTTTGGA	924	
Db	622	GCAATCAGAACTTTTGATCTCTGGAATATCAGCAGTGCCAAAATPACTGAACTTCATTTGGC	681	
Qy	925	AACTTCTTGATTGTTTCTCTTAAGTACCTTGTGTTGGTGTGCTGCAACCGGCTCTGATAAGT	984	
Db	682	AGTTTCTTTATCTGTTTCGGCTCCAGACCAATCTCTGGAGTAGCTTCTGGACTCTTTAGT	741	
Qy	985	GCATATGTTATCAAGAAAGCTATATTTGGAAGGCACTCAACTGACCGAGAGGTTGCCCTT	1044	
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ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE M (bases 1 to 651)
AUTHORS Motohashi, R., Shinozaki, K. and Yamaguchi-Shinozaki, K.
TITLE Arabidopsis thaliana YAC C1C3B1 region specific cDNA, clone 2
JOURNAL Unpublished (1999)
COMMENT Contact: Motohashi R
Laboratory of Plant Molecular Biology
Institute of Physical and Chemical Research (RIKEN)
3-1-1, Koyadai, Tsukuba 305-0074, Japan
Tel.: +81-298-36-4359
Email: motohasi@rtc.riken.go.jp.

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Query Match      27.3%; Score 595.6; DB 6; Length 651;
Best Local Similarity 98.2%; Pred. No. 8e-131;
Matches 640; Conservative 4; Mismatches 3; Indels 5; Gaps 4;

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QY 1285 ACACGGGACATCGATCGCAGTAGCTCAATCTTAATGGTCTGGTCATGGTTGGAAGA 1344
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QY 1345 GCAGGGTTCGTCTTCCGTTATCGTTTCTATCTACTTATGACCAAGAAATCAAGCGAG 1404
DB 121 GCAGGGTTCGTCTTCCGTTATCGTTTCTATCTACTTATGACCAAGAAATCAAGCGAG 180
QY 1405 AAAATCAATTTAATCATGAGGTTGTGATTTGGTGGTCTGGTCTCATGAGAGGTGCTGTA 1464
DB 181 AAAATCAATTTAATCATGAGGTTGTGATTTGGTGGTCTGGTCTCATGAGAGGTGCTGTA 240
QY 1465 TCTATGGCTCTGCATACAAAGTTTACAGGGCCGGGCACACAGATGTACGGGGAT 1524
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QY 1525 GCAATCATGATCAGCAGTACGATACTGTCTGTCTTTTATGACAGTGGTGTGTTGGTATG 1584
DB 301 GCAATCATGATCAGCAGTACGATACTGTCTGTCTTTTATGACAGTGGTGTGTTGGTATG 360
QY 1585 CTGACCAACCACTCATAGCTTACCTATTACCGCACCAAGACCGCCACACGAGCATGTTA 1644
DB 361 CTGACCAACCACTCATAGCTTACCTATTACCGCACCAAGACCGCCACACGAGCATGTTA 420
QY 1645 TCTGATGACCAACACCCCAAAATCCATACATATCCCTTTGTTGGACCAAGACTCGTTCAAT 1704
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RESULT 4
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CA767092
LOCUS AF53-Rpf_13_p08_T7_032.ab1 IRRI Drought Stress Panicle Library
DEFINITION Oryza sativa (indica cultivar-group) cDNA clone C0004976 5' similar
to Sodium/hydrogen exchanger 6 (Na(+)/H(+) exchanger 6) (NHE-6),
mRNA sequence.
CA767092
VERSION CA767092.2 GI:27549114
KEYWORDS EST.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretoidae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 834)
AUTHORS Bennett, J., Arumugam, K., Lafitte, R., Wen, J., Rudd, S. and
Bruskewich, R.M.
TITLE IRRI Drought Stress Panicle cDNA Library
JOURNAL Unpublished (2002)
COMMENT On Dec 2, 2002 this sequence version replaced gi:25996347.
Contact: Richard Bruskewich
Biometrics and Bioinformatics Unit
International Rice Research Institute
DAPO 7777, Metro Manila, Philippines
Tel: +63-2-845-0563
Fax: +63-2-845-0606
Email: r.bruskewich@cgiar.org
International Rice Information System (IRIS)
http://www.iris.irri.org: D0204975
Assignment of putative function to the sequence by S. Rudd of the
Munich Information Center for Protein Sequences
(http://mips.gsf.de)
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ORIGIN
Query Match      22.4%; Score 487.2; DB 6; Length 834;
Best Local Similarity 73.9%; Pred. No. 5.6e-105;
Matches 615; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

QY 760 GTATGTACATCGAGGTTCTCAATCAAGACGAGACACTTGTGCTTACAGTCTGTATTC 819
DB 2 GTCTGCACATTCGAGGTCCTCAATCAGATGAGACACCCCTTTTGTACAGTCTGTATTC 61
QY 820 GGAGAGGGTGTGTGAATGATGCAACGTCAGTCTGTGCTTCAACGGGATTCAGAGCTTT 879
DB 62 GGTGAAGGTGTGTGAACGATGCTACATCAATTGTGCTTTCAACGGCACTACAGACTTT 121
QY 880 GATCTCACTACCTAAACACGAAAGCTGCTTTTCATCTTCTTGGAAACTTCTTGTATTG 939
DB 122 GATCTTGTCCACATAGATGGGCTGTGCTTCTGAAATTCCTTGGGGAACCTCTTTATTTA 181
QY 940 TTTCTCTTAAGTACCTTGTGCTGCAACCGTCTGATAAGTGGTATGTTATCAAG 999
DB 182 TTTTGTGAGACACCTTCTTGGAGTATTTGCTGGATTCAGTGCATATATCAAG 241
QY 1000 AAGCTATACCTTTGGAAGGCACTCAACTGACCGAGAGGTGTGCCCTTATGATCTTATGCG 1059
DB 242 AAGCTATACATTTGGAAGGCACTTCTACTGACCGTGGGTTGCCCTTATGATCTATGGCT 301
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479	GTTAGCTCAATCTGTGGGTCTGTGTTTGGTGGAGGGCAGCAT	TGTGTTTCCCCCTG	538
1366	TGCTTTTCTATTCAACTTAGCCAAAGAAATCA	AAAGCGAGAAATCAACTTTAAACATGCAG	1425
539	TCATTTTGTCCAACTTGATGAAGAAGTCTCCGGAGGAGGAT	TAGCTTTTAACAGCAA	598
1426	GTGTGATTTGGTGTCTGGTCTCATAGAGGTGCTGTATCTAT	TATGGCTTTGGCATACAAC	1485
599	ATTATAATATGTGGGCTGGAACTTATCGAGGTGCTGTTT	CAGTGGCTCTGCTTTATAAT	658
1486	AAGTTTACAGGGCCGGGCACACAGATGTACGGGGAA	TGCANTCATGATCAGAGTACG	1545
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1724	ATGTGCTTCGGGCTTGACAGTATACGTGGCTTCT	TGTGACAGGGCCCACTCGAAACCGTGCATT	1783
899	ATGTACCCGGTCCCAAGTTTGGCGATGCTCCTAT	CAACACCATCTCAACACGTGCATC	958
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RESULT 8  
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 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

AV792419 433 bp mRNA linear EST 29-MAR-2002  
 AV792419 RAFL7 Arabidopsis thaliana CDNA clone RAFL07-14-P04 3',  
 mRNA sequence.  
 AV792419  
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 1 (bases 1 to 433)  
 Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,  
 Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,  
 Arkawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.  
 and Shinozaki, K.  
 Large scale analysis of Arabidopsis full-length cDNA (2002b)  
 Unpublished (2002)  
 Contact: Motoaki Seki  
 Plant Functional Genomics Research Group  
 RIKEN Genomic Sciences Center  
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
 Tel: 81-298-36-4359  
 Fax: 81-298-36-9060  
 Email: mseki@tc.riken.go.jp  
 An Arabidopsis full-length cDNA library was constructed essentially  
 as reported previously (Seki et al., 1998). cDNA cleaved with BamHI  
 and XhoI was ligated to modified lambda FLC-1 vector (Carninci et  
 al., submitted for publication) digested with BamHI and SalI. This  
 clone is in a modified pBluescript vector. Please visit our web

site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

#### FEATURES

source Location/Qualifiers

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#### ORIGIN

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Query Match 19.8%; Score 432; DB 1; Length 433;
Best Local Similarity 100.0%; Pred. No. 7.2e-92;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1718 ACCCAATGTCCTCGGCTGACAGTATACGTGGCTTTTGACACGGCCCACTCGAACCG 1777
D 433 ACCCAATGTCCTCGGCTGACAGTATACGTGGCTTTTGACACGGCCCACTCGAACCG 374
QY 1778 TGCATTACTCTGGAGACAAATTGATGACTCTTCATCGACCCCGCTCTTTGGAGGTGCTG 1837
D 373 TGCATTACTCTGGAGACAAATTGATGACTCTTCATCGACCCCGCTCTTTGGAGGTGCTG 314
QY 1838 GCTTTGTACCTTTGTTCCAGGTTCTCCAGTCTCCAGAGAAACCTCTCGATCTTAGTAAGG 1897
D 313 GCTTTGTACCTTTGTTCCAGGTTCTCCAGTCTCCAGAGAAACCTCTCGATCTTAGTAAGG 254
QY 1898 CTTGAGGTAACGTGGAGAAAGCTTTGATTTTGTGAGAAAGGGTGATTCAAAT 1957
D 253 CTTGAGGTAACGTGGAGAAAGCTTTGATTTTGTGAGAAAGGGTGATTCAAAT 194
QY 1958 TATGCTTTGTGTAATTAATTCATTTGTAATTAATTTGAGGACAGAAATCTGTCTTA 2017
D 193 TATGCTTTGTGTAATTAATTCATTTGTAATTAATTTGAGGACAGAAATCTGTCTTA 134
QY 2018 ACGTTTTCAGACAGAGAAACAAACATGCGCACTTTGAAAGTGTGTTGATGATGTA 2077
D 133 ACGTTTTCAGACAGAGAAACAAACATGCGCACTTTGAAAGTGTGTTGATGATGTA 74
QY 2078 TTATATTATATTTGTTTGTGTAACAAACTACACATTTGTTTATGTTTGAATTTG 2137
D 73 TTATATTATATTTGTTTGTGTAACAAACTACACATTTGTTTATGTTTGAATTTG 14
QY 2138 GTTTTGTCTTCG 2149
D 13 GTTTTGTCTTCG 2
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#### RESULT 9

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AV825792
LOCUS AV825792 RAFL7 Arabidopsis thaliana cDNA clone RAFL07-14-P04 5',
DEFINITION mRNA sequence.
ACCESSION AV825792
VERSION AV825792.1 GI:19867852
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 629)  
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.  
Large scale analysis of Arabidopsis full-length cDNA (2002b)  
Unpublished (2002)  
Contact: Motoaki Seki

TITLE  
JOURNAL  
COMMENT

Plant Functional Genomics Research Group

RIKEN Genomic Sciences Center

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-4359

Fax: 81-298-36-9060

Email: [meeki@rtc.riken.go.jp](mailto:meeki@rtc.riken.go.jp)

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLIC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

#### FEATURES

source Location/Qualifiers

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1..629
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL07-14-P04"
/dev_stage="rosette plants"
/lab_host="DH10B"
/clone_lib="RAFL7"
/note="Site 1: BamHI; Site 2: SalI; subjected to cold-treated (1, 2, 5, 10, 24 hr)"
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#### ORIGIN

```
Query Match 19.7%; Score 429.4; DB 1; Length 629;
Best Local Similarity 98.0%; Pred. No. 3.2e-91;
Matches 433; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCTCTCTGTTTCGTTCTCGTAGACGAGAGAGAAAGAAATCTCAGGTTTTAGCTTTTCCA 60
D 187 CCTCTCTGTTTCGTTCTCGTAGACGAGAGAGAGAAAGAAATCTCAGGTTTTAGCTTTTCCA 246
QY 61 AGCTTCCAAAATTTGAAATTTTGATCTTCTGGGCTCTTTTGTAAATCAGACTGAAGATAT 120
D 247 AGCTTCCAAAATTTGAAATTTTGATCTTCTGGGCTCTTTTGTAAATCAGACTGAAGATAT 306
QY 121 TTAGATTACCCAGAAAGTTGTTCAAGGAATGGTTTCAGTGACAGCAGCAGGAAAGATAAAG 180
D 307 TTAGATTACCCAGAAAGTTGTTCAAGGAATGGTTTCAGTGACAGCAGCAGGAAAGATAAAG 366
QY 181 AGACTTTTTCAGATTTTGTCTGATCCAAATCTGAATAGTTGTTTCATGTTCTTCTGGAT 240
D 367 AGACTTTTTCAGATTTTGTCTGATCCAAATCTGAATAGTTGTTTCATGTTCTTCTGGAT 426
QY 241 CAAATCTGGAAGAGGAAAGTTTGTGGATCTAGAGAAGATAACAATTTGGATTCTCTA 300
D 427 CAAATCTGGAAGAGGAAAGTTTGTGGATCTAGAGAAGATAACAATTTGGATTCTCTA 486
QY 301 GTGTCGAAACTGCTTCGTTATCGACATCTGATCAGCTTCTGTGGTTGCGTTGAATCTC 360
D 487 GTGTCGAAACTGCTTCGTTATCGACATCTGATCAGCTTCTGTGGTTGCGTTGAATCTC 546
QY 361 TTTGTCGACTTCTTGTGCTTGTATTGTTCTTCTGTCATCTTTTGGAGAGAGATAGATGG 420
D 547 TTTGTCGACTTCTTGTGCTTGTATTGTTCTTCTGTCATCTTTTGGAGAGAGATAGATGG 606
QY 421 ATGAACGAATCCATCACCCTCCT 442
D 607 ATGAACGAATCCATCACCCTCCT 628
```

#### RESULT 10

```
CD531888
LOCUS CD531888 12022 Arabidopsis Leaf Senescence Library Arabidopsis thaliana cDNA
DEFINITION 3', mRNA sequence.
ACCESSION CD531888
VERSION CD531888.1 GI:40451900
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsis.

## REFERENCE

1 (bases 1 to 448)

## AUTHORS

Guo, Y., Cai, Z. and Gan, S.

## TITLE

Transcriptome of Arabidopsis leaf senescence

## JOURNAL

Plant Cell Environ. 27 (5), 521-549 (2004)

## COMMENT

Contact: Susheng Gan

Department of Horticulture

Cornell University

119 Plant Science, Cornell University, Ithaca, NY 14853-5904, USA

Tel: 607 254 5418

Fax: 607 255 0599

Email: sg288@cornell.edu

Insert Length: 448 Std Error: 0.00

Seq primer: T7

POLYA=Yes.

## FEATURES

source

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/organism="Arabidopsis thaliana"

/mol\_type="mRNA"

/ecotype="Landsberg erecta"

/db\_xref="taxon:3702"

/tissue\_type="leaf"

/dev\_stage="yellow Leaf With Greenish Base Area"

/lab\_host="E. coli"

/clone\_lib="Arabidopsis Leaf Senescence Library"

/note="Organ: Rosette Leaf; Vector: pBluscript SKII+;

Site 1: EcoRI; Site 2: EcoRI; Senescent rosette leaves #5

and #6 (counted from the bottom) were harvested and

immediately frozen in liquid N2. The leaves were visibly

yellow excepted for the leaf base areas that were still

greenish."

greenish."

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greenish."

greenish."

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greenish."

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greenish."

BU004460

LOCUS

DEFINITION

QG55E06.yg.abi.QG.EFGHJ lettuce serriola Lactuca sativa cDNA clone

QG55E06, mRNA sequence.

ACCESSION

BU004460

VERSION

GI:22438855

KEYWORDS

EST.

SOURCE

ORGANISM

Lactuca sativa

Lactuca sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; campanulids; Asterales; Asteraceae; Cichorioideae;

Cichorieae; Lactuca.

1 (bases 1 to 733)

Kozik, A., Micheltore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,

Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,

Elison, P., Kollman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,

Lai, Z., Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project

http://compgenomics.ucdavis.edu/

Unpublished (2002)

Contact: Alexander Kozik [R.W.Micheltore]

Department of Vegetable Crops, R.W.Micheltore Lab

University of California at Davis (UCD)

Amundson Hall, UCD, Davis, CA 95616, USA

Tel: 1-(530)-742-1742

Fax: 1-(530)-752-9659

Email: akozik@ucdavis.org [micheltore@vegmail.ucdavis.edu]

belongs to contig QG\_CA\_Contig6585, see http://cgdb.ucdavis.edu/

for details.

Plate: QGGS row: E column: 06.

Location/Qualifiers

1..733

/organism="Lactuca sativa"

/mol\_type="mRNA"

/cultivar="L.serriola"

/db\_xref="taxon:4236"

/clone="QG5E06"

/lab\_host="E.coli"

/clone\_lib="QG\_EFGHJ lettuce serriola"

/note="Vector: pBRCDNA51AB; The library was constructed

from 10 different sources of RNA from a single genotype.

Separate cDNAs were generated using primers that

incorporated unique 5' and 3' tags to distinguish each

source of RNA. cDNAs were then pooled, size-fractionated,

directionally cloned into a custom medium-copy vector and

transformations made with four size classes to minimize

size bias. Details of each source of RNA and library

construction can be obtained at http://cgdb.ucdavis.edu/

TAG\_TISSUE=flowers environmental stress

TAG\_LIB=QG\_EFGHJ lettuce serriola

TAG\_SEQ=CGAATGCGGG"

## ORIGIN

Query Match

Best Local Similarity

Matches 518; Conservative

19.1%; Score 416.6; DB 5;

Length 733;

Pred. No. 3.7e-88;

Mismatches 169; Indels

0; Gaps

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

BU004460

LOCUS

DEFINITION

QG55E06.yg.abi.QG.EFGHJ lettuce serriola Lactuca sativa cDNA clone

QG55E06, mRNA sequence.

ACCESSION

BU004460

VERSION

GI:22438855

KEYWORDS

EST.

SOURCE

ORGANISM

Lactuca sativa

Lactuca sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; campanulids; Asterales; Asteraceae; Cichorioideae;

Cichorieae; Lactuca.

1 (bases 1 to 733)

Kozik, A., Micheltore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,

Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,

Elison, P., Kollman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,

Lai, Z., Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project

http://compgenomics.ucdavis.edu/

Unpublished (2002)

Contact: Alexander Kozik [R.W.Micheltore]

Department of Vegetable Crops, R.W.Micheltore Lab

University of California at Davis (UCD)

Amundson Hall, UCD, Davis, CA 95616, USA

Tel: 1-(530)-742-1742

Fax: 1-(530)-752-9659

Email: akozik@ucdavis.org [micheltore@vegmail.ucdavis.edu]

belongs to contig QG\_CA\_Contig6585, see http://cgdb.ucdavis.edu/

for details.

Plate: QGGS row: E column: 06.

Location/Qualifiers

1..733

/organism="Lactuca sativa"

/mol\_type="mRNA"

/cultivar="L.serriola"

/db\_xref="taxon:4236"

/clone="QG5E06"

/lab\_host="E.coli"

/clone\_lib="QG\_EFGHJ lettuce serriola"

/note="Vector: pBRCDNA51AB; The library was constructed

from 10 different sources of RNA from a single genotype.

Separate cDNAs were generated using primers that

incorporated unique 5' and 3' tags to distinguish each

source of RNA. cDNAs were then pooled, size-fractionated,

directionally cloned into a custom medium-copy vector and

transformations made with four size classes to minimize

size bias. Details of each source of RNA and library

construction can be obtained at http://cgdb.ucdavis.edu/

TAG\_TISSUE=flowers environmental stress

TAG\_LIB=QG\_EFGHJ lettuce serriola

TAG\_SEQ=CGAATGCGGG"

Query Match

Best Local Similarity

Matches 518; Conservative

19.1%; Score 416.6; DB 5;

Length 733;

Pred. No. 3.7e-88;

Mismatches 169; Indels

0; Gaps

0;

0;

0;

0;

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0;

0;

BU004460

LOCUS

DEFINITION

QG55E06.yg.abi.QG.EFGHJ lettuce serriola Lactuca sativa cDNA clone

QG55E06, mRNA sequence.

ACCESSION

BU004460

VERSION

GI:22438855

KEYWORDS

EST.

SOURCE

ORGANISM

Lactuca sativa

Lactuca sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; campanulids; Asterales; Asteraceae; Cichorioideae;

Cichorieae; Lactuca.

1 (bases 1 to 733)

Kozik, A., Micheltore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,

Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,

Elison, P., Kollman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,

Lai, Z., Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower EST

```
QY 563 ATGCAAGGTTTCAAGTAAAGAGAGACAGTTTTCGCAATTTTCGTGCTATTATGCTTT 622
Db 287 ATGCTGGGTTTCAGGTTAAGAAAGAACAAATTTTTTCGCAATTTTCATGACCAATTGTCAT 346
QY 623 TTGCTGCTGTTGGGACTATTATTTCTTGCAATCATATCTCTAGGTGTAACACAGATTCT 682
Db 347 TTGCTGCTGTTGGCACTGTGATATCTTTCACCATCATATCATTTGGTGTCTAATAATTT 406
QY 683 TTAAGAAGTTGACATGGAACCTTTGACTTGGGTGATATCTTCTGCTATTGGTGCATAT 742
Db 407 TCCAAGAGTGTGATGTTGTAACCTTGAGCTTGGAGACTTTCTTGCAATTTGGTGAATAT 466
QY 743 TTGCTGCAACAGATTCACTATGATGCACTGCAAGTTCTGNAATCAAGACAGACCTTTGC 802
Db 467 TTTAGCACCAAGATTCCGTTTGGCACTTTGCAAGTGTGAAATCAGGATCAGACACCTTTAT 526
QY 803 TTTACAGTCTTGTATTTCGAGAGGGTGTGTGAATGATGCAACGTCAGTTGTGGTCTTCA 862
Db 527 TATATAGTTTGGTGTGTTGGTGAAGTGTGGTGAATGATGCCACATCATGTTGTCACTTCA 586
QY 863 AGCGAATTCAGAGCTTTGATCTCATCTACCTAAACCAACCAAGCTCTTTTTCATCTTTG 922
Db 587 ATGCAAGTTCAAACTTTGATCTCTCTCAAAATCACAACCTGCTGTGCAATTTCAACTGATT 646
QY 923 GAAACTCTTGTATTTGTTTCTCCTAAGTACCTGCTGTTGGTGTGCAACCGTCTGATAA 982
Db 647 GAAATTTCTTTATTTATTTATTCATCAAGACACATTTCTAGGAGCTGGAGCTGGGCTACTAA 706
QY 983 GTGCTATGTTTATCAAGAGCTATATCT 1009
Db 707 GTGCTATATTAAGAAGCTATATTT 733
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CO094724
LOCUS GR_Ea17A01.r GR_Ea Gossypium raimondii cDNA clone GR_Ea17A01 3',
mRNA sequence.
CO094724.1 GI:48793410
ACCESSION EST.
VERSION CO094724.1
KEYWORDS Gossypium raimondii
SOURCE Gossypium raimondii
ORGANISM Gossypium raimondii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 827)
Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C.,
Udall, J. A., Rapp, R. A., Wendel, J. F., Rao, K., Soderlund, C. and
Wing, R. A.
Global assembly of Cotton ESTs
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
Plate1 17 row: A column: 01.
FEATURES
1..827
Location/Qualifiers
1..827
/organism="Gossypium raimondii"
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/dev_stage="first true leaves"
/lab_host="DH10B"
/clone_lib="GR_Ea"
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EcoRV; Library made by Invitrogen with RNA supplied by
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Wendle lab. Directional cloned into NotI-EV. Colonies
plated/picked by AGI. More glycerol clones held in -80."
ORIGIN
Query Match 19.1%; Score 416.2; DB 7; Length 827;
Best Local Similarity 70.5%; Pred. No. 4.7e-88;
Matches 556; Conservative 0; Mismatches 233; Indels 0; Gaps 0;
QY 973 GGTCTGATAGAGTGGGTATGTTATCAAGAAGCTATACCTTTGGAAAGGCACTCAACATGACCGA 1032
Db 37 GGGTTGGTTAGTGTTCATCATCAAAAAGTTGACTTTTGGAAAGGCACTCAACAGATCGT 96
QY 1033 GAGGTGCGCTTATGATGCTTATGCGCTATCTTTCTTATATGCTTGTGAGCTTTTCGAC 1092
Db 97 GAATTTGCTCTTATGATGCTTATGGCATACCTTTTCGTATATCATGGCTGAACCTGTTCTAT 156
QY 1093 TTGAGCGGTATTCCTCACTGTGTTTTCTGTGGTATTGTGATGTCCCATTAACATATGGCAC 1152
Db 157 TTGAGTGGCATTTCTCAGATATTCTTTTGTGGGATTTGTGATGCATATACCTGGCAC 216
QY 1153 AATGTAAACGGAGAGCTCAAGAATAACAACAAGCATACCTTTTGGCACTTTGTGCTATTTCTT 1212
Db 217 AATGTTACAGAGAGTTCAAGAGATTACTACAAGCATGCTTTGTCTACCTTGTCTCATTTGTT 276
QY 1213 GCGGAGACATTTATTTCTTGTATGTTGGAATGATGCTTTGGACATTTGACATGAGAGGAGA 1272
Db 277 GCTGAGACTTTTCTTTCTTTTATGTCGGGATGATGCTTTGGACATGGAGAGTGGAGA 336
QY 1273 TCCGTGATGACACACCGGAAACATCGATCGAGTGAGCTCAATCCTTAATGGGTCTCGTGC 1332
Db 337 TTTGTCAGTGATAGCCCTCGGAACGTGCTGCTTAGTGTGCTGATGGGTCTTGT 396
QY 1333 ATGTTTGAAGAGAGAGCGTTCGCTTTCCGTTATTCGTTTCTATCTAATCTTAGCCAAAGAG 1392
Db 397 ATGCTTGGAGAGAGAGCTTTTGTGTTTCCCTGTCATTTTATCCAACTTTGGCAAAAGAA 456
QY 1393 AATCAAGCGAGAGAAATCAACTTTTAAACATGACAGCTTGTGATTTGCTGTGCTCTCATG 1452
Db 457 TCAGCTAGTGAATAAATCAGCTTCAGGGAACAAATTATATATGTTGGTCTGGGCTCATG 516
QY 1453 AGAGGTGCTGTATCTATGGCTCTTTGCATACAACAAGTTTACAAGGGCGGGSCACACAGAT 1512
Db 517 AGAGGCTGTATCTATGGCACTTTGCATATAAATCAGTTTACAAGGGGGGCCATACCTAG 576
QY 1513 GTAGCGGGAATGAATCATGATCAGCAGTACGATACTGTCTGCTTTTGTAGCAGCAGTG 1572
Db 577 TTGCGAGGAAATGCAATTATGATTTACAAGCACTATAACCAATTTGTTCTATTTCAGCAGCTGT 636
QY 1573 GTGTTTGTGTGCTGACCAACCACTCATAGCTACCTATTACCGCACCAAGACGCCACC 1632
Db 637 GTTTTGTGTTTATGACTTAACCTCTTAATAGGTTCTTGTGCCACATCCCAAAACCAACA 696
QY 1633 ACAGAGCATGTTTATCTGATGACAAACACCCCAAAATCCATACATATCCCTTTTGTGGACCA 1692
Db 697 GCCAGCATGCTCTCAGACCAATCTACTCCAAAATCAATGGAGGCCACCATTTCTCGGAAGC 756
QY 1693 GACTCGTTTCATGAGCCCTTCAGGGAACCAATGTGCTCGCTGACAGTATACGTGGC 1752
Db 757 GGCCAGGATTTCTTTTGTATGATAGTTTAAATGGAGTTTCATCGACCAAAACAGCATTTCTGTGCA 816
QY 1753 TTCTTTGACA 1761
Db 817 CTCTTTACA 825
```

```
RESULT 13
BE420587
LOCUS BE420587
DEFINITION HM000.D12 ITEC HWM Barley Leaf Library Hordeum vulgare subsp.
vulgare cDNA clone HM000.D12, mRNA sequence.
ACCESSION BE420587
VERSION BE420587.1
KEYWORDS BE420587.1 GI:9418430
EST.
```

SOURCE  
ORGANISM  
Hordeum vulgare subsp. vulgare  
Hordeum vulgare subsp. vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Hordeum.  
1 (bases 1 to 1212)  
Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T.,  
Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A.,  
Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J.,  
Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P.,  
Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G.,  
Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G.  
International Triticeae EST Cooperative (ITEC): Production of  
Expressed Sequence Tags for Species of the Triticeae  
Unpublished (2000)  
Contact: Herrmann RG  
Botanisches Institut der LMU  
Menzinger Str. 67, D-80638 Munchen GERMANY  
Fax: 49 30 171683  
Email: herrmann@botanik.biologie.uni-muenchen.de  
International Triticeae EST Cooperative (ITEC)  
http://wheat.pw.usda.gov/genome.  
Location/Qualifiers  
1. .1212  
/organism="Hordeum vulgare subsp. vulgare"  
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/cultivar="barke"  
/sub\_species="vulgare"  
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/clone="HWM000.D12"  
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/note="Vector: pBluescriptSK(-); 850 bp average insert  
size."

Query Match 19.1%; Score 415.8; DB 2; Length 1212;  
Best Local Similarity 69.1%; Pred. No. 6.2e-88;  
Matches 614; Conservative 0; Mismatches 267; Indels 8; Gaps 3;

QY 587 AGCAGTTTTCGCAATTTGTCGATATTATGCTTTTGGTCTGTTGGACATATTATTT 646  
DB 61 AACAATTTTCGCAATTTTCATGACTATTACATTTGTTCCGTTAGTTGGACCTGATCT 120  
QY 647 CTTCGCAATCATATCTCTAGGTGTAACAGCTTCTTTAAGAGTTGGACATGGAACCT 706  
DB 121 CCTTCAGTATAATATCACTTGGTGGCCATGGGGCTAGTATCAAGGCTGAACATAGGCGCC 180  
QY 707 TTGACTTGGGTGATTATCTTGCTATTGGTGCCATATTGCTGCAACAGATTTCAGTATGTA 766  
DB 181 TTGAGCTTGGAGACTACCTGCACTTGGGGCAATATTCTGGCAACGGACTCTTCGCA 240  
QY 767 CACTGCAGTTCTGAATCAAGACGACACCTTTGCTTTACAGTCTTTGTTATCGGAGAGG 826  
DB 241 CCTTGCAGGTGTTAAGCAAGATGACACACCTTTCTTGACAGTTTGGTGGTGAAG 300  
QY 827 GTGTTGTGAATGATGCAAGTCAGTTGTGCTTCAACCGATTTCAGCTTTGATCTCA 886  
DB 301 GTGTTGTTAAGCATGCGACATGATGTTGTGTTCAATGCAATTCAGAACTTTGATCTTG 360  
QY 887 CTCACCTAAACCAAGAGCTGCTTTTCATCTTCTGGAACTTCTTGATTTGTTCTCC 946  
DB 361 GAAATTTAGTAGCTCAAAATCTTCAATTCATGGAATTTCTCTATCTATTGTTGGG 420  
QY 947 TAAGTACCTTGGTGTGTCGAACCGGTCTGATAGTGGCTGATGTTATCAAGAACTAT 1006  
DB 421 CCAGTACCTTTCTTGGAGTATCTAGTGGAATCTCTAGTCTTATGTCATCAAGAACTGT 480  
QY 1007 ACTTTGGAAGGCACTCAACTGACCGAGAGTTGCCCTTATGATGCTTATGGGCTATCTTT 1066  
DB 481 ACTTTGGCAGGCACTCCACTGATCGTGAAGTTGCTATTATGATGCTCATGGCTTATTTAT 540

ORIGIN  
Query Match 19.1%; Score 415; DB 7; Length 827;

QY 1067 CTTATATGCTTGTGCTGAGCTTTTCGACTTTCGAGCGGTATCTCTACTGTGTTTCTGTGTA 1126  
DB 541 CTTATATGCTGCTGCTGAATTTGCTTGTGTTGAGTGGTATTCTCAGCGTTTCTTCTGTGTA 600  
QY 1127 TTGTGATGTCCTCATACATGCGACATGTAACGAGAGCTCAAGATAACAACAAGC 1186  
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QY 1187 ATACCTTTGCAACTTTGTCATTTCTTCTGGGACACATTTATTTCTTGTATGTTGAATCG 1246  
DB 661 ATGCTTTTGGCAATGTCATCTCTGAGACGTTTCTCTTCTTATGTTGGCATGG 720  
QY 1247 ATGCTTTTGGCAATGTCATCTCTGAGAGTCCGTCAGTG-----ACACACCGGGAACATCGAT 1301  
DB 721 ATGCAATTCGATATAGAGAGTGGAAATTTGGTAGTGAACATATAGCCCAATGAATCTAT 780  
QY 1302 CGCAGTGAGCTCAATCTTAATGGGTCTGTCATGTTGGAAGACGAGCGTTCGTCTTTCC 1361  
DB 781 TGCCTTGGAGCTCATTTATTTTGGCGTGTGTCGTTGCAAGAGCTGCAATTTGTTTCC 840  
QY 1362 GTTATGCTTTCTATCTAACTTAGCCAAAGAAATCAAAACGAGAAATCAACTTTTAACAT 1421  
DB 841 TCTATCTATCTCTCC--AATTGACCAAAAATACTCCAGCGGAAGATCTCTGTTAGGCA 898  
QY 1422 GCAGGTTGTGATTTGGTGTCTGCTCTCATGAGAGTGTCTGTCATCTATG 1470  
DB 899 GCAAGTTATTTTGTGGGCG--GGGCTCATGAGAGGGGCGGTGTCATG 946

RESULT 14  
LOCUS CO085721  
DEFINITION GR\_Ea03A21.f GR\_Ea Gossypium raimondii cDNA clone GR\_Ea03A21 5',  
mRNA sequence.  
ACCESSION CO085721  
VERSION CO085721.1 GI:48776355  
KEYWORDS EST.  
SOURCE Gossypium raimondii  
ORGANISM Gossypium raimondii  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
1 (bases 1 to 827)  
Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C.,  
Udall, J.A., Rapp, R.A., Wendel, J.F., Rao, K., Soderlund, C. and  
Wing, R.A.  
Global assembly of Cotton ESTs  
Unpublished (2004)  
Contact: Rod A. Wing  
Arizona Genomics Institute  
The University of Arizona  
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: http://genome.arizona.edu  
Plate: 03 row: A column: 21.  
Location/Qualifiers  
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/lab\_host="DH10B"  
/clone\_lib="GR\_Ea"  
/note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:  
EcoRV; Library made by Invitrogen with RNA supplied by  
Wendle lab. Directional cloned into NotI-EV. Colonies  
plated/picked by AGI. More glycerol clones held in -80."

ORIGIN  
Query Match 19.1%; Score 415; DB 7; Length 827;



Best Local Similarity 71.3%; Pred. No. 9e-88;  
Matches 547; Conservative 0; Mismatches 220; Indels 0; Gaps 0;

QY 880 GATCTCAGTCACTAAACACGAGCTGCTTTTCATCTCTTGGAACTCTTGTATTTG 939  
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QY 940 TTTCTCCTAAGTACCTTGTGCTGCTCAACCGCTCTGATAAGTGCCTATCTTATCAAG 999  
Db 61 TTCACTCAGCTACTTTGCTAGAGTGTGACTGCACTGCTCAGTGTCTTCAATATTA 120  
QY 1000 AAGCTATCTTTGGAAGCACTCAACTGACCGAGAGTGTGCTTTATGATGCTTATGGCG 1059  
Db 121 AAGCTGTATTTGGAAGCACTCAACTGATCGAGAGTGTGCTTTATGATGCTCATGGCT 180  
QY 1060 TATCTTTCTATATGCTGCTGAGCTTTTCGACTTTGAGGGTATCCTCAGTGTGTTTTTC 1119  
Db 181 TACCTCTCATACATGCTGCTGAACTTTTCTATTTAAGCGGAATTTCTTACAGTATCTTT 240  
QY 1120 TGTGCTATTGCTATGCTCCCATTTACATGCGCAATGTAAACGAGAGCTCAAGATAACA 1179  
Db 241 TGTGGATTTGATGCTCACTATACATGGGCATATGTTACGAAAGTTCAAGAGTGACA 300  
QY 1180 ACAAGCATACCTTTTGCACTTTGTCACTTTCTTGGCGAGACATTTATTTCTTGTATGTT 1239  
Db 301 ACAAGCATGCTTTTGTCTACTTATCACTTTGTTGCTGAGATCTTTATCTTCTCTATGTT 360  
QY 1240 GGAATGGATGCTTGGACATTTGACAAAGTGGAGATCCGTGAGTGACACACCGGGAACATCG 1299  
Db 361 GGTATGGATGCTTTGGACATCGAGAAGTGGAGATTTATCAGTGATAGCCCGGAAATCA 420  
QY 1300 ATCGAGTGAAGTCAATCTAATGCTGCTGGTCACTGTTTGAAGAGAGCGTTCGTCCTTT 1359  
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Db 661 AGCAACAATCAGCTGTTCTTTTTCAGACAGTGGTTTTTCGGATTGATGACTAACCATT 720  
QY 1600 ATAAGCTATCTATACCGACACAGAACGCCACCAAGAGATGTTATC 1646  
Db 721 GTTAGGATCTGCTTCTCTCCAAAACATCTCTCGAGAATGCTTTC 767

RESULT 15  
CB681657  
LOCUS  
DEFINITION  
OSJNEf08D05.f OSJNEf Oryza sativa (japonica cultivar-group) cDNA  
clone OSJNEf08D05 5', mRNA sequence.  
ACCESSION  
CB681657  
VERSION  
CB681657.1  
KEYWORDS  
GI:29685382  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
1 (bases 1 to 852)  
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,  
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.  
Large-scale identification of ESTs involved in the interaction

JOURNAL  
COMMENT

between rice and Magnaporthe grisea  
Unpublished (2003)  
Contact: Rod Wing  
Arizona Genomics Institute  
University of Arizona  
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ  
85721-0088, USA  
Tel: 520 626 3967  
Fax: 520 621 9288  
Email: http://genome.arizona.edu  
PCR Primers  
FORWARD: gta aaa cga cgg cca gtc  
BACKWARD: gga aac agc tat gac cat g  
Plate: 08 row: D column: 05  
Seq primer: gta aaa cga cgg cca gtc.  
location/Qualifiers

FEATURES  
source

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XhoI; Uninfected Control"

ORIGIN

Query Match 19.0%; Score 414.2; DB 6; Length 852;  
Best Local Similarity 67.9%; Pred. No. 1.4e-87;  
Matches 578; Conservative 0; Mismatches 273; Indels 0; Gaps 0;

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QY 805 TACAGTCTTGATTCGGAGAGGGTGTGTGAATGATCAACCTCAGTTGTGGTCTTCAAC 864  
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QY 865 GCGATTCAAGCTTTGATCTCCTCACTAAACCAACGAAAGCTGCTTTTCATCTTTTGGGA 924  
Db 182 GCAATTGAAGACATTTGATATTGCTAAATTTTGATAGCCTTGTCTACTAGCGTTTCATAG 241  
QY 925 AACTTCTTGATTTGTTTCTCTTAAGTACCTTGTGCTTGGTGTGCTGCAACCGGCTCTGATAGT 984  
Db 242 AATTTTCTCTACCTATTCTTCCACAGTACCTTCTTGGAGTAGTGTGCTGGGTGCTTAGT 301  
QY 985 GCGTATGTTATCAAGAAGCTATCTTTTGAAGGACACTCAACTGACCGAGAGTTGCCCTT 1044  
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QY 1045 ATGATGCTTATGGCGTATCTTTTCTTATATGCTTCTGAGCTTTTCGACTTTGAGCGGTATC 1104  
Db 362 ATGATCTCATGGCGTACCTTTTCATATATGCTGCGATGCTGCTAGATCTGAGTGGCAT 421  
QY 1105 CTCACTGTTTTTCTGTTGTTGTTGATGTCCTCCATTTACATGCGACACATGTAACGGAG 1164  
Db 422 CTCACTGTTTCTTCTCTGGAATAGTAAATGTCACATTTACACTTGGCATTAATGTGACAGAA 481  
QY 1165 AGCTCAAGAATAACAACAAGCACTCTTTGCAACTTTGTCTTCTTTGCGGAGACATTT 1224  
Db 482 AGCTCTAGGATTAATACCAAGCACACCTTTTGCTACTTTTCTTCTTCTGCTGAATTTT 541  
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Qy 1285 ACACCGGAAACATCGATCGAGTGAAGCTCAATCTAATGGTCTGGTCAATGGTGGAGA 1344  
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Qy 1345 GCAGCGTTCTGCTCTTTCCGTTATCGTTTCTATCTAAGTGAAGGAGGAGGAGGAG 1404  
Db |||||  
Qy 662 GCAGCATTTGTTATTCCTTTGCTTTTATCCAAATCTAAGTAAAAAGAGACAGCCCA 721  
Db |||||  
Qy 1405 AAAATCAACTTTAAACATGCAGGTTGTGATTTGGTGGTCTGCTCATGAGAGGTGCTGA 1464  
Db |||||  
Qy 722 AAGATCTCTTCAAGCAGCAAGTAATCATATGGTGGCAGGTCTCATGAGAGGAGGAGTA 781  
Db |||||  
Qy 1465 TCTATGGCTCTTGCATACAAAGTTTACAAGGGCCGGGCACACAGATGTACCGGGAAT 1524  
Db |||||  
Qy 782 TCAATAGCACTTGGCTTATCACAAGTTTCCCGCATCTGGTCACTGAAATTCGGAATCAT 841  
Db |||||  
Qy 1525 GCAATCATGAT 1535  
Db |||||  
Qy 842 GCTATCATGAT 852  
Db |||||

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Job time : 7209 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2005, 22:06:40 ; Search time 1181 Seconds  
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10917.186 Million cell updates/sec

Title: US-10-617-624-1

Perfect score: 2178

Sequence: 1 cctctctgttctgtctctgcg.....aaaaaaaaaaaaaaaaaaaaa 2178

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- N\_Geneseq\_16Dec04:\*
- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2178	100.0	2178	2	Aaz22591 Arabidops
2	2143.4	98.4	2284	2	Aaz22595 Arabidops
3	1617	74.2	1617	6	Abz13434 Arabidops
4	1617	74.2	1617	12	Adn74230 Thale cre
5	1614	74.1	1614	12	Adn11979 Wild type
6	1612.4	74.0	1614	12	Adn11981 AtHNX1 mu
7	1563	71.8	1563	12	Adn11983 AtHNX1 mu
8	1563	71.8	1566	12	Adn11989 AtHNX1 mu
9	1473	67.6	1473	12	Adn11985 AtHNX1 mu
10	1407	64.6	1410	12	Adn11991 NDL-2 enc
11	1362	62.5	1362	12	Adn11987 AtHNX1 mu
12	1320.4	60.6	1323	12	Adn11993 NDL-3 enc
13	848	38.9	1449	12	Adm68265 Plant Na+
14	832.8	38.2	1568	3	Aaz72926 Atlliplex
15	821.2	37.7	2553	4	Aaf75765 Gene regu
16	813	37.3	2423	4	Aaf75764 Gene regu
17	806.4	37.0	1668	6	Acc49921 Suaeda sa
18	806.4	37.0	2397	6	Acc49920 Suaeda sa
19	805.4	37.0	1315	12	Adm68266 Arabidops
20	797.6	36.6	1620	10	Adj99891 Potato sa

21	794.4	36.5	1621	10	ADJ99890
22	774.8	35.6	2237	4	Aaf75752 Gene regu
23	768.8	35.3	2330	3	Aaa61876 cDNA encd
24	754.4	34.6	2361	4	Aaf75766 Gene regu
25	682.6	31.3	1638	10	ACF58165
26	651	29.9	1955	11	ADM82830
27	523.8	24.0	1788	2	Aaz222592
28	491.6	22.6	1674	6	ABK12638
29	418	19.2	418	8	ABX62293
30	401.8	18.4	1740	12	ADM68263
31	269.2	12.4	612	13	ACN53419
32	252.6	11.6	330	2	Aaz222611
33	226.4	10.4	378	2	Aaz222606
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35	165.2	7.6	466	12	ADP94869
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37	153.2	7.0	588	10	ADD17689
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ALIGNMENTS

RESULT 1

Aaz22591

ID Aaz22591 standard; cDNA; 2178 BP.

XX AC Aaz22591;

XX DT 18-JAN-2000 (first entry)

XX DE Arabidopsis thaliana Na/H transporter gene AtNHX1.

XX KW Sodium; proton; antiport; transporter; salt tolerance; salt management;

XX KW transgenic plant; survival; soil; farming; accumulation; irrigation;

XX KW crop; ss.

XX OS Arabidopsis thaliana.

XX PN WO9947679-A2.

XX PD 23-SEP-1999.

XX PF 18-MAR-1999; 99WO-CA000219.

XX PR 18-MAR-1998; 98US-0078474P.

XX PR 15-JAN-1999; 99US-0116111P.

XX (BLUM/) BLUMWALD E.

XX (APSE/) APSE M.

XX (SNED/) SNEDDEN W.

XX (AHAR/) AHARON G.

XX Blumwald E, Apse M, Snedden W, Aharon G;

XX WPI; 1999-571840/48.

XX P-PSDB; AAY40901.

XX Nucleic acid molecules encoding sodium/proton transport polypeptides,

XX useful in genetic engineering salt tolerance in crop plants.

XX Claim 4; Fig 1A; 93pp; English.

XX The invention relates to an isolated nucleic acid molecule encoding a

XX plant Na/H antiport (PNHX) transporter polypeptide, or a fragment and

XX capable of increasing salt tolerance in a cell. This sequence corresponds

CC to the gene encoding the AtNHX1 transporter from Arabidopsis thaliana.  
CC The Na/H transporter polypeptides provide a means of intracellular salt  
CC management, particularly in plants. the sequences are useful for  
CC producing transgenic plants that are capable of surviving in soil with  
CC high salt levels that would normally inhibit growth of the crop species.  
CC This would be useful in farming land in areas that are generally  
CC considered unproductive through salt accumulation and poor irrigation,  
CC e.g. in India, Australia, and prairies in USA or Canada. Commercial  
CC crops, such as potatoes, tomatoes, brassica, cotton, sunflower,  
CC strawberries, spinach, lettuce, rice, soybean, corn, wheat, rye, barley,  
CC atriplex, sorghum, alfalfa, salicornia and others would benefit from  
CC increased salt tolerance  
XX  
SQ Sequence 2178 BP; 576 A; 413 C; 472 G; 717 T; 0 U; 0 Other;

Query Match 100.0%; Score 2178; DB 2; Length 2178;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 361 TTTGTTGACACTCTTTGCTGTTATGTTCTTGGTCTCTTTTGGAGAGAAATAGATGG 420

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QY 601 AATTTTCGTGACTATTATGCTTTTGGTCTGTTGGGACTATTATTTCTTGACAAATCATATA 660  
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DB 781 AATCAAGACGACACCTTTGCTTTTACAGTCTTTGATTTCCGAGAGGGTGTGTGAATGAT 840  
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QY 1681 TTGTTGGACCAAGACTCGTTTCAATTTGAGCTTTCAGGAAACCAATGTGCTCGGCTGAC 1740  
DB 1681 TTGTTGGACCAAGACTCGTTTCAATTTGAGCTTTCAGGAAACCAATGTGCTCGGCTGAC 1740

QY 1741 AGTATACGTGGCTTCTTGACACGCGCCCATCTCGAACCCTGCAATTTACTACTGAGACAATTT 1800  
DB 1741 AGTATACGTGGCTTCTTGACACGCGCCCATCTCGAACCCTGCAATTTACTACTGAGACAATTT 1800

QY 1801 GATCACTCTCTCATGCGACCCGCTTTTGGAGGTGCTGCTTTTGTACCTTTGTTCCAGGT 1860  
DB 1801 GATCACTCTCTCATGCGACCCGCTTTTGGAGGTGCTGCTTTTGTACCTTTGTTCCAGGT 1860

QY 1861 TCTCAACTGAGAGAAACCCCTCTCTGATCTTAGTAGGCTTGAAGGTTAAAGGGAAGAAA 1920  
DB 1861 TCTCAACTGAGAGAAACCCCTCTCTGATCTTAGTAGGCTTGAAGGTTAAAGGGAAGAAA 1920

QY 1921 GCTTTGATTTTTTTGGTAGAAAAGGGTGATTCAAATATATGCTTTTGTGTAATATATCCA 1980  
DB |||||||  
1921 GCTTTGATTTTTTTGGTAGAAAAGGGTGATTCAAATATATGCTTTTGTGTAATATATCCA 1980  
QY 1981 TTTGTAATATTTTGTGAGGACAGAAATCTCTTAACGTTTTCAGAGCAGAAAGCAAA 2040  
DB |||||||  
1981 TTTGTAATATTTTGTGAGGACAGAAATCTCTTAACGTTTTCAGAGCAGAAAGCAAA 2040  
QY 2041 ACATGCGCACTTTGAAGTGTGTTGATGTATGTAATATATATTCATATTTCTTTTGTG 2100  
DB |||||||  
2041 ACATGCGCACTTTGAAGTGTGTTGATGTATGTAATATATATTCATATTTCTTTTGTG 2100  
QY 2101 TTAACACAACTACACATTTTATGTTTGTGATTTGTTTCTTCGAAAAA 2160  
DB |||||||  
2101 TTAACACAACTACACATTTTATGTTTGTGATTTGTTTCTTCGAAAAA 2160  
QY 2161 AAAAAA 2178  
DB |||||||  
2161 AAAAAA 2178

RESULT 2

AZ22595  
ID AZ22595 standard; cDNA; 2284 BP.  
XX AC  
XX AZ22595;  
DT 18-JAN-2000 (first entry)  
XX  
DE Arabidopsis thaliana Na/H transporter gene.  
XX  
XX Sodium; proton; antiport; transporter; salt tolerance; salt management;  
KW transgenic plant; survival; soil; farming; accumulation; irrigation;  
KW crop; ss.  
XX

OS Arabidopsis thaliana.

PN WO947679-A2.

XX 23-SEP-1999.

PF 18-MAR-1999; 99WO-CA000219.

XX 18-MAR-1998; 98US-0078474P.

PR 15-JAN-1999; 99US-011611P.

XX (BLUM/) BLUMWALD E.

PA (APSE/) APSE M.

PA (SNED/) SNEDDEN W.

PA (AHAR/) AHARON G.

XX Blumwald E, Apse M, Snedden W, Aharon G;

XX WPI; 1999-571840/48.

DR P-PSDB; AAY40905.

XX Nucleic acid molecules encoding sodium/proton transport polypeptides,

XX useful in genetic engineering salt tolerance in crop plants.

PS Claim 48; Fig 5A-B; 93pp; English.

XX The invention relates to an isolated nucleic acid molecule encoding a  
CC plant Na/H antiport (PNHX) transporter polypeptide, or a fragment and  
CC capable of increasing salt tolerance in a cell. This sequence corresponds  
CC to the gene encoding a transporter from Arabidopsis thaliana. The Na/H  
CC transporter polypeptides provide a means of intracellular salt  
CC management, particularly in plants. The sequences are useful for  
CC producing transgenic plants that are capable of surviving in soil with  
CC high salt levels that would normally inhibit growth of the crop species.  
CC This would be useful in farming land in areas that are generally  
CC considered unproductive through salt accumulation and poor irrigation,  
CC e.g. in India, Australia, and prairies in USA or Canada. Commercial

CC crops, such as potatoes, tomatoes, brassica, cotton, sunflower,  
CC strawberries, spinach, lettuce, rice, soybean, corn, wheat, barley,  
CC atriplex, sorghum, alfalfa, salicornia and others would benefit from  
CC increased salt tolerance  
XX  
SQ Sequence 2284 BP; 589 A; 444 C; 485 G; 766 T; 0 U; 0 Other;  
Query Match 98.4%; Score 2143.4; DB 2; Length 2284;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2166; Conservative 0; Mismatches 1; Indels 2; Gaps 2;  
QY 1 CCTCTCTGTTTCGTTCTCTGAGCAAGAAAGAAAGAAATCTCAGGTTTAGCTTTTCA 60  
DB |||||||  
116 CCTCTCTGTTTCGTTCTCTGAGCAAGAAAGAAAGAAATCTCAGGTTTAGCTTTTCA 175  
QY 61 AGCTTCCAAAATTTTGAATTTTGTCTCGGCTCTTTTGTAAATCAGACTGGAAGATAT 120  
DB |||||||  
176 AGCTTCCAAAATTTTGAATTTTGTCTCTCGGCTCTTTTGTAAATCAGACTGGAAGATAT 235  
QY 121 TTAGATTACCCAGAAAGTTGTTCAAGGAATGTTTTCAGTGGACAGCACGGAAGATAAAG 180  
DB |||||||  
236 TTAGATTACCCAGAAAGTTGTTCAAGGAATGTTTTCAGTGGACAGCACGGAAGATAAAG 295  
QY 181 AGACTTTTTCAGATTTTCTGATCCAAAATCTGAATAGTTGTTTCATGTTCTTGGAT 240  
DB |||||||  
296 AGACTTTTTCAGATTTTCTGATCCAAAATCTGAATAGTTGTTTCATGTTCTTGGAT 355  
QY 241 CAAATCTGGAAGAGGAAGTTTGTGGATCTAGAAAGAGATAACAATGTTGGATTCTCTA 300  
DB |||||||  
356 CAAATCTGGAAGAGGAAGTTTGTGGATCTAGAAAGAGATAACAATGTTGGATTCTCTA 415  
QY 301 GTGTGAAATGCTTTCGTTATCGACATCTGATCAACGCTTCTGTGGTTGCGTTGAATCTC 360  
DB |||||||  
416 GTGTGAAATGCTTTCGTTATCGACATCTGATCAACGCTTCTGTGGTTGCGTTGAATCTC 475  
QY 361 TTTGTTGCACTTCTTTGTGCTTGTATTTGTTCTTGTGTCATCTTTTGGAAAGAGATAGTG 420  
DB |||||||  
476 TTTGTTGCACTTCTTTGTGCTTGTATTTGTTCTTGTGTCATCTTTTGGAAAGAGATAGTG 535  
QY 421 ATGAACGAATCCATCACCGCTTGTGTTGTTGGCTTAGGCACCTGGTGTACCAATTTGTTG 480  
DB |||||||  
536 ATGAACGAATCCATCACCGCTTGTGTTGTTGGCTTAGGCACCTGGTGTACCAATTTGTTG 595  
QY 481 ATTAGTAAAGAAAAGCTCGCATCTTCTCTCTTTTAGTGAAGATCTTTTCTTCATATAT 540  
DB |||||||  
596 ATTAGTAAAGAAAAGCTCGCATCTTCTCTCTTTTAGTGAAGATCTTTTCTTCATATAT 655  
QY 541 CTTTGGCACCCTTATATTCATGCAAGGTTTCAAGTAAAGAAAGAACAGCTTTTCCGC 600  
DB |||||||  
656 CTTTGGCACCCTTATATTCATGCAAGGTTTCAAGTAAAGAAAGAACAGCTTTTCCGC 715  
QY 601 AATTTCGTGACTATTATGCTTTTGGTCTGTTGGGACTATTATTCTTGCAATCATATA 660  
DB |||||||  
716 AATTTCGTGACTATTATGCTTTTGGTCTGTTGGGACTATTATTCTTGCAATCATATA 775  
QY 661 TCTCTAGGTGTAACACAGTTCTTTTAAAGAGTTGGAACATTTGGAACCTTTGACTTGGGTGAT 720  
DB |||||||  
776 TCTCTAGGTGTAACACAGTTCTTTTAAAGAGTTGGAACATTTGGAACCTTTGACTTGGGTGAT 835  
QY 721 TATCTTGCTATTTGGTCCATATTTGTCGAACAGATTCAGTATGATGACTGCAAGTTCTG 780  
DB |||||||  
836 TATCTTGCTATTTGGTCCATATTTGTCGAACAGATTCAGTATGATGACTGCAAGTTCTG 895  
QY 781 AATCAAGACGAGACACCTTTCTTACAGTCTTGTATTTCGAGAGGGTGTGTGAATGAT 840  
DB |||||||  
896 AATCAAGACGAGACACCTTTCTTACAGTCTTGTATTTCGAGAGGGTGTGTGAATGAT 955  
QY 841 GCAAGCTCAGTTGGTCTTCAAGCGGATTCAGAGCTTTGATCTCAGTCACTCAACCAACAC 900  
DB |||||||  
956 GCAAGCTCAGTTGGTCTTCAAGCGGATTCAGAGCTTTGATCTCAGTCACTCAACCAACAC 1015  
QY 901 GAAGCTGTTTCACTTTCTTGGAAACCTTCTGTATTGTTGTTTCTCCTAAGTACCTTGTT 960  
DB |||||||





QY 346 GTTGGTGAATCTCTTTGTGCACTCTTTGTGCTGTGTAATGTTCTTGGTCACTTTTG 405  
DB |||||  
61 GTTGGTGAATCTCTTTGTGCACTCTTTGTGCTGTGTAATGTTCTTGGTCACTTTTG 120  
QY 406 GAAGAGATAGATGATGAACAAATCCATCACCGCTTGTGTAATGTTGGCTAGGCACTGGT 465  
DB |||||  
121 GAAGAGATAGATGATGAACAAATCCATCACCGCTTGTGTAATGTTGGCTAGGCACTGGT 180  
QY 466 GTTACCAATTTGTTGATTAAGTAAAGGAAAGCTCGCATCTTCTCGTCTTTAGTGAAGAT 525  
DB |||||  
181 GTTACCAATTTGTTGATTAAGTAAAGGAAAGCTCGCATCTTCTCGTCTTTAGTGAAGAT 240  
QY 526 CTTTCTTCATATATCTTTTGGCCACCAATTAATTAATGCAAGGTTTCAAGTAAAAAAG 585  
DB |||||  
241 CTTTCTTCATATATCTTTTGGCCACCAATTAATTAATGCAAGGTTTCAAGTAAAAAAG 300  
QY 586 AAGCAGTTTTCGGCAATTTCTGACTATTATGCTTTTGTGCTGTTGGGACTATTATT 645  
DB |||||  
301 AAGCAGTTTTCGGCAATTTCTGACTATTATGCTTTTGTGCTGTTGGGACTATTATT 360  
QY 646 TCTTGCACAATCATATCTCTAGTGTAAACACAGTTCTTTAAGAAAGTTGACATTCGAACC 705  
DB |||||  
361 TCTTGCACAATCATATCTCTAGTGTAAACACAGTTCTTTAAGAAAGTTGACATTCGAACC 420  
QY 706 TTTGACTTTGGGTGATTAATCTGCTATTTGGTGCCATATTTGCTGCAACAGATTCAATATGT 765  
DB |||||  
421 TTTGACTTTGGGTGATTAATCTGCTATTTGGTGCCATATTTGCTGCAACAGATTCAATATGT 480  
QY 766 ACACGTGAGGTTCTGAATCAAGACAGACACCTTTGCTTTTAAAGTCTTGTATTCGGAGAG 825  
DB |||||  
481 ACACGTGAGGTTCTGAATCAAGACAGACACCTTTGCTTTTAAAGTCTTGTATTCGGAGAG 540  
QY 826 GGTGTTGTGAATGATGCAACGTGAGTTGGTCTTCAACGGGATTCAGAGCTTTCATCTC 885  
DB |||||  
541 GGTGTTGTGAATGATGCAACGTGAGTTGGTCTTCAACGGGATTCAGAGCTTTCATCTC 600  
QY 886 ACTCACCTAAACACGAGCTCTTTTTCATCTTCTTGGAACTTCTTGTATTTGTTTCTC 945  
DB |||||  
601 ACTCACCTAAACACGAGCTCTTTTTCATCTTCTTGGAACTTCTTGTATTTGTTTCTC 660  
QY 946 CTAAGTACCTTCTGCTGCTGCAACCGTCTGATAAGTGCATATGTTATCAAGAAGCTA 1005  
DB |||||  
661 CTAAGTACCTTCTGCTGCTGCAACCGTCTGATAAGTGCATATGTTATCAAGAAGCTA 720  
QY 1006 TACTTTGGAAGGCACTCAACTCACGAGAGGTTGCCCTTATGATCTTATGCGGTATCTT 1065  
DB |||||  
721 TACTTTGGAAGGCACTCAACTCACGAGAGGTTGCCCTTATGATCTTATGCGGTATCTT 780  
QY 1066 TCTTATATGCTTGTGAGCTTTTTCGACTTTGAGCGGTATCTCCTCACTGTGTTTCTGTGCT 1125  
DB |||||  
781 TCTTATATGCTTGTGAGCTTTTTCGACTTTGAGCGGTATCTCCTCACTGTGTTTCTGTGCT 840  
QY 1126 ATTGTGATGTCCATTTACATGCGACAAATGTAACGAGAGCTCAAGAATTAACAACAAG 1185  
DB |||||  
841 ATTGTGATGTCCATTTACATGCGACAAATGTAACGAGAGCTCAAGAATTAACAACAAG 900  
QY 1186 CATACCTTGCAACTTGTCTTCTTGGGAGACATTTATTTCTTGTATGTTGGAATG 1245  
DB |||||  
901 CATACCTTGCAACTTGTCTTCTTGGGAGACATTTATTTCTTGTATGTTGGAATG 960  
QY 1246 GATGCTTTGGACATTTGACAAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1305  
DB |||||  
961 GATGCTTTGGACATTTGACAAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1020  
QY 1306 GTGAGCTCAATCCTTAATGGTCTGTCTGCTTCTTGGGAGAGAGCGTTCTGCTTTCCGTTA 1365  
DB |||||  
1021 GTGAGCTCAATCCTTAATGGTCTGTCTGCTTCTTGGGAGAGAGCGTTCTGCTTTCCGTTA 1080  
QY 1366 TCGTTTCTATCTAACTTAGCCCAAGAGATCAAGCGGGAATCAACTTTAAGATGAG 1425  
DB |||||  
1081 TCGTTTCTATCTAACTTAGCCCAAGAGATCAAGCGGGAATCAACTTTAAGATGAG 1140  
QY 1426 GTTGTGATTTGGTGTCTGCTCATGAGAGGTGCTGATCTATGCTCTTGCATACAAAC 1485

DB |||||  
1141 GTTGTGATTTGGTGTCTGGTCTCATGAGAGGTGCTGTATCTATGGCTCTTGCATACAAC 1200  
QY 1486 AAGTTTAAAGGGCGGGCACACAGATGTACGGGGATGCAATCATCATCAACGATACG 1545  
DB |||||  
1201 AAGTTTAAAGGGCGGGCACACAGATGTACGGGGATGCAATCATCATCAACGATACG 1260  
QY 1546 ATAACTGCTCTCTTTTGTAGCACAGTGTGTTTGGTATGCTGACCAAAACCACTCATAGC 1605  
DB |||||  
1261 ATAACTGCTCTCTTTTGTAGCACAGTGTGTTTGGTATGCTGACCAAAACCACTCATAGC 1320  
QY 1606 TACCTATTACCGCACAGAAACCGCACAGCATGTTATCTGATGACAAACCCCAAAA 1665  
DB |||||  
1321 TACCTATTACCGCACAGAAACCGCACAGCATGTTATCTGATGACAAACCCCAAAA 1380  
QY 1666 TCCATACATATCCCTTTTGGACCAAGACTCGTTTCTTATGAGCCCTTCAGGGNAACCAAT 1725  
DB |||||  
1381 TCCATACATATCCCTTTTGGACCAAGACTCGTTTCTTATGAGCCCTTCAGGGNAACCAAT 1440  
QY 1726 GTGCTCGGCTGACAGTATACGTGGCTTTTGACACGGCCCACTCGAAACCGTGCATTAC 1785  
DB |||||  
1441 GTGCTCGGCTGACAGTATACGTGGCTTTTGACACGGCCCACTCGAAACCGTGCATTAC 1500  
QY 1786 TACTGGAGACAATTTGATGACTCTCTTCAATCGACCCCGTCTTTGGAGGTGCTGGCTTTGTA 1845  
DB |||||  
1501 TACTGGAGACAATTTGATGACTCTCTTCAATCGACCCCGTCTTTGGAGGTGCTGGCTTTGTA 1560  
QY 1846 CCTTTTGTTCAGGTTCTTCCAACTGAGAGAAACCCCTCTCTGATCTTAGTAGGCTTGA 1902  
DB |||||  
1561 CCTTTTGTTCAGGTTCTTCCAACTGAGAGAAACCCCTCTCTGATCTTAGTAGGCTTGA 1617

## RESULT 4

ADN74230

ID ADN74230 standard; cDNA; 1617 BP.

XX AC ADN74230;

XX DT 15-JUL-2004 (first entry)

XX DE Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 2125.

XX KW gene; ss; plant; transgenic; E2Fa/Dpa transcription factor;

XX KW growth regulator; animal feed product; thale cress;

XX KW cell wall biosynthesis; nitrogen metabolism; carbon metabolism.

XX OS Arabidopsis thaliana.

XX PN WO2004035798-A2.

XX PD 29-APR-2004.

XX PF 20-OCT-2003; 2003WO-EP011658.

XX PR 18-OCT-2002; 2002EP-00079408.

XX XX (CROP-) CROPDISEGN NV.

XX XX Inze D, De Veylder L, Vlieghe K;

XX XX WPI; 2004-348466/32.

XX XX P-PSDB; ADN74231.

XX PT Altering plant characteristics, useful for producing plants for enzyme or  
XX PT pharmaceutical production comprises modifying in a plant, expression of  
XX PT one or more nucleic acids and/or modifying level or activity of one or  
XX PT more proteins.

XX PS Claim 1; SEQ ID NO 2125; 134pp; English.

XX CC This invention relates to a novel method for altering one or more plant

XX CC characteristics. Specifically, it refers to identifying genes that are up

XX CC - or down-regulated in transgenic plants overexpressing the heterodimeric

CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to  
 CC alter plant characteristics accordingly. The present invention describes  
 CC generating transgenic plants for the production of growth regulators,  
 CC enzymes, therapeutics, pharmaceuticals and animal feed products, where  
 CC the altered plant characteristics are selected from increased yield or  
 CC biomass, enhanced survival capacity, stress tolerance, plant architecture  
 CC or physiology, altered endoreduplication, biochemistry, signal  
 CC transduction, storage lipid mobilisation and/or altered photosynthesis,  
 CC each relative to the corresponding wild type plants. Accordingly, these  
 CC sequences can also be useful as positive or negative selectable markers  
 CC during transformation of cells or tissues. The identified genes play a  
 CC role in a variety of biological processes such as DNA replication, cell  
 CC wall biosynthesis, nitrogen and/ or carbon metabolism or they function as  
 CC transcription factors. This polynucleotide sequence is thale cress cDNA  
 CC repressed 1.3 fold or more in plants overexpressing the E2Fa/Dpa  
 CC transcription factor, given in an exemplification of the invention.  
 XX

SQ Sequence 1617 BP; 389 A; 346 C; 359 G; 523 T; 0 U; 0 Other;

Query Match 74.2%; Score 1617; DB 12; Length 1617;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 286 ATGTTGGATTCTCTAGTGTGAAACTGCTTCGTTATCGACATCTGATCAGCGCTTCGTG 345  
 DB 1 ATGTTGGATTCTCTAGTGTGAAACTGCTTCGTTATCGACATCTGATCAGCGCTTCGTG 60

QY 346 GTTGGTTGAATCTCTTTGTTGCACTCTTTGTGCTTGATATGTTCTTTGGTCATCTTTTG 405  
 DB 61 GTTGGTTGAATCTCTTTGTTGCACTCTTTGTGCTTGATATGTTCTTTGGTCATCTTTTG 120

QY 406 GAAGAGATAGATGATCAAGATCCATCACCGCTTGTGATTTGGCTAGGCACTGCT 465  
 DB 121 GAAGAGATAGATGATCAAGATCCATCACCGCTTGTGATTTGGCTAGGCACTGCT 180

QY 466 GTTACCATTTGTTGATTAGTAAAGAAAAAGCTCGCATCTTCTCGTCTTTAGTGAAGAT 525  
 DB 181 GTTACCATTTGTTGATTAGTAAAGAAAAAGCTCGCATCTTCTCGTCTTTAGTGAAGAT 240

QY 526 CTTTCTTCATATATCTTTTGGCCACCATATATATCAATGACGGTTTCAAGTAAAAAAG 585  
 DB 241 CTTTCTTCATATATCTTTTGGCCACCATATATATCAATGACGGTTTCAAGTAAAAAAG 300

QY 586 AAGCAGTTTTCCGCAATTCGTGACTATATGCTTTTGTGCTGCTTTGGCACTATTATT 645  
 DB 301 AAGCAGTTTTCCGCAATTCGTGACTATATGCTTTTGTGCTGCTTTGGCACTATTATT 360

QY 646 TCTTGCACAATCATATCTCTAGGTGTAAACAGATTTCTTTAAGAAAGTTGGACATTTGAACC 705  
 DB 361 TCTTGCACAATCATATCTCTAGGTGTAAACAGATTTCTTTAAGAAAGTTGGACATTTGAACC 420

QY 706 TTTGACTTGGGTGATATCTTGCTATTGGTGCCATATTTGCTGCAACAGATTCAGTATGT 765  
 DB 421 TTTGACTTGGGTGATATCTTGCTATTGGTGCCATATTTGCTGCAACAGATTCAGTATGT 480

QY 766 ACATGCAAGTTCTGAATCAAGACAGACACTTTGCTTTACGTCCTGTATTTCGGAGAG 825  
 DB 481 ACATGCAAGTTCTGAATCAAGACAGACACTTTGCTTTACGTCCTGTATTTCGGAGAG 540

QY 826 GGTGTGTGAATGATGCAACGTCAGTTGCTGTGTTCTTCAACGGGATTCAGAGCTTTGATCTC 885  
 DB 541 GGTGTGTGAATGATGCAACGTCAGTTGCTGTGTTCTTCAACGGGATTCAGAGCTTTGATCTC 600

QY 886 ACTACCTAAACCAAGAGCTGCTTTTCATCTTCTTTGGAAAACCTTCTTGTTATTTGTTCTC 945  
 DB 601 ACTACCTAAACCAAGAGCTGCTTTTCATCTTCTTTGGAAAACCTTCTTGTTATTTGTTCTC 660

QY 946 CTAGTACTTGTGTTGGTCTGCAACCGTCTGTAAGTGGTATGTTATCAAGAGCTA 1005  
 DB 661 CTAGTACTTGTGTTGGTCTGCAACCGTCTGTAAGTGGTATGTTATCAAGAGCTA 720

QY 1006 TACTTTGGAAGGCACTCAAACTGACCGAGAGGTTGCCCTTATGATGCTTTATGGCGTATCTT 1065

DB 721 TACTTTGGAAGGCACTCAAACTGACCGAGAGGTTGCCCTTATGATGCTTATGGCGTATCTT 780  
 QY 1066 TCTTATATGCTTGTGAGCTTTTTCGACTTGAGCGGTATCCTCACTGTGTTTCTTGTTG 1125  
 DB 781 TCTTATATGCTTGTGAGCTTTTTCGACTTGAGCGGTATCCTCACTGTGTTTCTTGTTG 840  
 QY 1126 ATTCTGATGTCCCATTTACATGSCACAATGTAAACGAGAGCTCAAGAATAACACAAAG 1185  
 DB 841 ATTCTGATGTCCCATTTACATGSCACAATGTAAACGAGAGCTCAAGAATAACACAAAG 900  
 QY 1186 CATACCTTTGCAACTTTTGTGCTTTCTTTCGCGAGACATTTATTTCTTGTATGTTGGAATG 1245  
 DB 901 CATACCTTTGCAACTTTTGTGCTTTCTTTCGCGAGACATTTATTTCTTGTATGTTGGAATG 960  
 QY 1246 GATCCCTTGGACATTTGACATGAGATCCGTGAGTGACACACCGGGAACATCCATCGCA 1305  
 DB 961 GATCCCTTGGACATTTGACATGAGATCCGTGAGTGACACACCGGGAACATCCATCGCA 1020  
 QY 1306 GTGAGCTCAATCCTTAATGGGTCTGCTCATGTTTGAAGAGCAGCGTTTCGTTCCGTTA 1365  
 DB 1021 GTGAGCTCAATCCTTAATGGGTCTGCTCATGTTTGAAGAGCAGCGTTTCGTTCCGTTA 1080  
 QY 1366 TCGTTTCTATCTACTTACTAGCCAAAGAAATCAAAAGCGAGAAAAATCAAATTTAAACATG 1425  
 DB 1081 TCGTTTCTATCTACTTACTAGCCAAAGAAATCAAAAGCGAGAAAAATCAAATTTAAACATG 1140  
 QY 1426 GTTGTGATTTGGTGGTCTGCTCATGAGAGGTGCTGTATCTATGCTCTTTCGATACAAAC 1485  
 DB 1141 GTTGTGATTTGGTGGTCTGCTCATGAGAGGTGCTGTATCTATGCTCTTTCGATACAAAC 1200  
 QY 1486 AAGTTTACAAGGGCGGGCACACAGATGTACGGGGAAATGCAATCATGATCAGAGTACG 1545  
 DB 1201 AAGTTTACAAGGGCGGGCACACAGATGTACGGGGAAATGCAATCATGATCAGAGTACG 1260  
 QY 1546 ATAACTGCTGTCTTTTGTAGCACAGTGGTGTGTTGGTATGCTGACCAAAACCACTCATAGC 1605  
 DB 1261 ATAACTGCTGTCTTTTGTAGCACAGTGGTGTGTTGGTATGCTGACCAAAACCACTCATAGC 1320  
 QY 1606 TACCTATTACGGCACAGAACGCCACACGAGCATGTTATCTGATGACACACACCCCAAAA 1665  
 DB 1321 TACCTATTACGGCACAGAACGCCACACGAGCATGTTATCTGATGACACACACCCCAAAA 1380  
 QY 1666 TCCATACATATCCCTTTTGGACCAAGACTCGTTTCAATGAGCCCTTCAGGGAAACCAAT 1725  
 DB 1381 TCCATACATATCCCTTTTGGACCAAGACTCGTTTCAATGAGCCCTTCAGGGAAACCAAT 1440  
 QY 1726 GTGCTCGGCTGACAGTATACGTGGCTTCTTGACACGGGCCACTCGAAACCGTGCATPAC 1785  
 DB 1441 GTGCTCGGCTGACAGTATACGTGGCTTCTTGACACGGGCCACTCGAAACCGTGCATPAC 1500  
 QY 1786 TACTGGAGACATTTGATGACTCCTTCATGCGACCCCTCTTTGGAGGTCTGGGCTTTGTA 1845  
 DB 1501 TACTGGAGACATTTGATGACTCCTTCATGCGACCCCTCTTTGGAGGTCTGGGCTTTGTA 1560  
 QY 1846 CCCTTTGCTTCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTAGTAAAGGCTTGA 1902  
 DB 1561 CCCTTTGCTTCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTAGTAAAGGCTTGA 1617

RESULT 5  
 ADN11979  
 ID ADN11979 standard; DNA; 1614 BP.  
 XX  
 AC ADN11979;  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE Wild type AtNHX1 encoding sequence.  
 XX  
 KW salt tolerance; Na+/H+ transporter polypeptide; AtNHX1; ds.  
 XX  
 OS Arabidopsis thaliana.  
 XX

Key Location/Qualifiers

FT CDS 1.1614

FT /tag= a

FT /product= "AtNHX1"

XX WO2004007668-A2.

XX 22-JAN-2004.

XX 09-JUL-2003; 2003WO-US021549.

XX 12-JUL-2002; 2002US-0395662P.

XX (REGC ) UNIV CALIFORNIA.

XX Shi H, Blumwald E;

XX WPI: 2004-122911/12.

XX P-PSDB; ADN11980.

PT Enhancing salt tolerance of a plant comprises introducing into the plant a polynucleotide encoding a Na<sup>+</sup>/H<sup>+</sup> transporter polypeptide.

XX Disclosure; SEQ ID NO 1; 38pp; English.

CC The present invention relates to enhancing salt tolerance of a plant comprises introducing into the plant a polynucleotide encoding a Na<sup>+</sup>/H<sup>+</sup> transporter polypeptide. The AtNHX1 gene confers salt tolerance. The composition and methods are useful in conferring salt, tolerance on plants and other organisms. The present sequence represents wild type AtNHX1 encoding sequence.

XX Sequence 1614 BP; 388 A; 346 C; 358 G; 522 T; 0 U; 0 Other;

Query Match 74.1%; Score 1614; DB 12; Length 1614;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1614; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 286 ATGTGGATCTCTAGTGTGAAAGTGGCTTGTATCGACATCTGATCAGCTTCTGTG 345

DB 1 ATGTGGATCTCTAGTGTGAAAGTGGCTTGTATCGACATCTGATCAGCTTCTGTG 60

QY 346 GTTGGTGAATCTCTTTGTGCACTCTTTGTGCTGTGATTTGTTCTTTGGTCACTTTTG 405

DB 61 GTTGGTGAATCTCTTTGTGCACTCTTTGTGCTGTGATTTGTTCTTTGGTCACTTTTG 120

QY 406 GAAGAGATAGATGATGAACGAATCCATCACCCTTTGTTGATTTGGCTAGGCACTGT 465

DB 121 GAAGAGATAGATGATGAACGAATCCATCACCCTTTGTTGATTTGGCTAGGCACTGT 180

QY 466 GTTACCAATTTGTTAGTAAAGGAAAGCTCGCATCTCTCTGTTAGTGAAGAT 525

DB 181 GTTACCAATTTGTTAGTAAAGGAAAGCTCGCATCTCTCTGTTAGTGAAGAT 240

QY 526 CTTTCTTCATATATCTTTTGGCCACCAATATATTCAATGCAAGGGTTTCAAGTAAAAAG 585

DB 241 CTTTCTTCATATATCTTTTGGCCACCAATATATTCAATGCAAGGGTTTCAAGTAAAAAG 300

QY 586 AAGCAGTTTTCGCAATTTGCTGACTATATGCTTTTGGTCTGTTGGGCACTATTATT 645

DB 301 AAGCAGTTTTCGCAATTTGCTGACTATATGCTTTTGGTCTGTTGGGCACTATTATT 360

QY 646 TCTTGCACATCATATCTTAGTGTAAACAGTTTCTTTTAAAGAGTTGCAATTTGGAACC 705

DB 361 TCTTGCACATCATATCTTAGTGTAAACAGTTTCTTTTAAAGAGTTGCAATTTGGAACC 420

QY 706 TTTGACTTTGGGTGATTTATCTTGTATTTGGTGTGCATATTTTGTGCAACAGATTCAGTATGT 765

DB 421 TTTGACTTTGGGTGATTTATCTTGTATTTGGTGTGCATATTTTGTGCAACAGATTCAGTATGT 480

QY 766 ACATGCAAGTTTCTGAATCAAGACAGACACCTTTTGTCTTTACGTTCTTTGATTCGAGAG 825

DB 481 ACATGCAAGTTTCTGAATCAAGACAGACACCTTTTGTCTTTACGTTCTTTGATTCGAGAG 540

QY 826 GGTGTTGTAATGATGCAACGTCAGTGTGCTTCAACGCGATTCAGAGCTTTGATCTC 885

DB 541 GGTGTTGTAATGATGCAACGTCAGTGTGCTTCAACGCGATTCAGAGCTTTGATCTC 600

QY 886 ACTACCTAAACACGAGAGCTGCTTTTCACTTTTGGAAACTCTTGTATTTGTTTCTC 945

DB 601 ACTACCTAAACACGAGAGCTGCTTTTCACTTTTGGAAACTCTTGTATTTGTTTCTC 660

QY 946 CTAAGTACCTTTGCTTGGTGTGCAACGCTGTGAAGTGTGATTTATCAAGAGCTA 1005

DB 661 CTAAGTACCTTTGCTTGGTGTGCAACGCTGTGAAGTGTGATTTATCAAGAGCTA 720

QY 1006 TACTTTGGAAGGCACTCAACTGACGAGAGGTTCCTTTATGATGCTTTATGCGTATCTT 1065

DB 721 TACTTTGGAAGGCACTCAACTGACGAGAGGTTCCTTTATGATGCTTTATGCGTATCTT 780

QY 1066 TCTTATATGCTTGTGAGCTTTTTCGACTTGAAGCGGTATCTCTCACTGTGTTTCTGTG 1125

DB 781 TCTTATATGCTTGTGAGCTTTTTCGACTTGAAGCGGTATCTCTCACTGTGTTTCTGTG 840

QY 1126 ATTGTGATGTCCTTATACACATGTCACAACTCTTAACGAGAGCTCAAGATTAACAAAG 1185

DB 841 ATTGTGATGTCCTTATACACATGTCACAACTCTTAACGAGAGCTCAAGATTAACAAAG 900

QY 1186 CATACCTTTGCAACTTTTGTCACTTTTTCGCGAGACATTTATTTCTGTATGTTGGAATG 1245

DB 901 CATACCTTTGCAACTTTTGTCACTTTTTCGCGAGACATTTATTTCTGTATGTTGGAATG 960

QY 1246 GATGCTTTGGACATTTGCAACTGAGATTCCTGATGTGACACACCGGGAACATCGATCGCA 1305

DB 961 GATGCTTTGGACATTTGCAACTGAGATTCCTGATGTGACACACCGGGAACATCGATCGCA 1020

QY 1306 GTGAGCTCAATCTTAATGGGCTGCTGTCATGCTGCGAGAGAGAGCTTCTTCCGTTA 1365

DB 1021 GTGAGCTCAATCTTAATGGGCTGCTGTCATGCTGCGAGAGAGAGCTTCTTCCGTTA 1080

QY 1366 TCGTTTCTATCTAACTTAGCCAAAGAAATCAAGCGAGAAATCAACTTTTAAACATGAG 1425

DB 1081 TCGTTTCTATCTAACTTAGCCAAAGAAATCAAGCGAGAAATCAACTTTTAAACATGAG 1140

QY 1426 GTTGTGATTTGGTGTGCTCTCATGAGAGGTGCTGTATCTATGGCTCTTGTGATACAC 1485

DB 1141 GTTGTGATTTGGTGTGCTCTCATGAGAGGTGCTGTATCTATGGCTCTTGTGATACAC 1200

QY 1486 AAGTTTACAGGGCGGGGACACAGATGTACGCGGAGTCAATCATGATCACGAGTACG 1545

DB 1201 AAGTTTACAGGGCGGGGACACAGATGTACGCGGAGTCAATCATGATCACGAGTACG 1260

QY 1546 ATAACTGTCTGCTTTTGTAGCAGAGTGTGTTTGTGATGCTGACCCAAACCACTCATAGC 1605

DB 1261 ATAACTGTCTGCTTTTGTAGCAGAGTGTGTTTGTGATGCTGACCCAAACCACTCATAGC 1320

QY 1606 TACCTATTACCGCACACGAGCGCCACACGAGCATGTTATCTGATGACAAACCCCAAAA 1665

DB 1321 TACCTATTACCGCACACGAGCGCCACACGAGCATGTTATCTGATGACAAACCCCAAAA 1380

QY 1666 TCCATACATATCCCTTTTGGACCAAGACTCGCTTCTTGTGAGCTTTCAGGGAACCAAT 1725

DB 1381 TCCATACATATCCCTTTTGGACCAAGACTCGCTTCTTGTGAGCTTTCAGGGAACCAAT 1440

QY 1726 GTGCTCGGCTGACAGTATACAGTGGCTTCTTGTAGACGCGCCACTCGAACCGTGCATTAC 1785

DB 1441 GTGCTCGGCTGACAGTATACAGTGGCTTCTTGTAGACGCGCCACTCGAACCGTGCATTAC 1500

QY 1786 TACTGGAGACAAATTTGATGACTCTTTCATGCGACCCGCTTTTGGAGGTCTGTTGTTGTA 1845

DB 1501 TACTGGAGACAAATTTGATGACTCTTTCATGCGACCCGCTTTTGGAGGTCTGTTGTTGTA 1560

QY 1846 CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTTAGTAGGCT 1899

DB 1561 CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTTAGTAGGCT 1614

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RESULT 6
ADN11981
ID ADN11981 standard; DNA; 1614 BP.
XX AC
XX ADN11981;
XX
XX 17-JUN-2004 (first entry)
XX
XX ATHX1 mutant encoding sequence #1.
XX DE
XX salt tolerance; Na+/H+ transporter polypeptide; AtNHX1; ds.
XX OS
XX Synthetic.
XX
XX WO2004007668-A2.
XX
XX 22-JAN-2004.
XX
XX 09-JUL-2003; 2003WO-US021549.
XX
XX 12-JUL-2002; 2002US-0395662P.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX PA
XX Shi H, Blumwald E;
XX
XX WPI; 2004-122911/12.
XX
XX P-PSDB; ADN11982.
XX
XX Enhancing salt tolerance of a plant comprises introducing into the plant
XX a polynucleotide encoding a Na+/H+ transporter polypeptide.
XX
XX Claim 17; SEQ ID NO 3; 38pp; English.
XX
XX The present invention relates to enhancing salt tolerance of a plant
XX comprises introducing into the plant a polynucleotide encoding a Na+/H+
XX transporter polypeptide. The AtNHX1 gene confers salt tolerance. The
XX composition and methods are useful in conferring salt tolerance on plants
XX and other organisms. The present sequence represents a mutant AtNHX1
XX encoding sequence.
XX
XX Sequence 1614 BP; 388 A; 345 C; 359 G; 522 T; 0 U; 0 Other;

Query Match      74.0%; Score 1612.4; DB 12; Length 1614;
Best Local Similarity 99.9%; Pred. NO. 0;
Matches 1613; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 286 ATGTTGGATTCTCTAGTGTGAAAGTGCCTTCGTTATCGACATCTGATCAGCTTCTGTG 345
DB 1 ATGTTGGATTCTCTAGTGTGAAAGTGCCTTCGTTATCGACATCTGATCAGCTTCTGTG 60

QY 346 GTTGGTTGAATCTCTTTGTTGCACTTCTTTGTGCTTGTATTTGTTGTTGTCATCTTTTG 405
DB 61 GTTGGTTGAATCTCTTTGTTGCACTTCTTTGTGCTTGTATTTGTTGTTGTCATCTTTTG 120

QY 406 GAAGAGATAGATGATGAAGCAATCCATCCACCGCTTTGTTGATTTGGCTAGGCACTGGT 465
DB 121 GAAGAGATAGATGATGAAGCAATCCATCCACCGCTTTGTTGATTTGGCTAGGCACTGGT 180

QY 466 GTTACCATTTGTTGATTAGTAAGGAAAAGCTCGCATCTCTCGTCTTTAGTGAAGAT 525
DB 181 GTTACCATTTGTTGATTAGTAAGGAAAAGCTCGCATCTCTCGTCTTTAGTGAAGAT 240

QY 526 CTTTCTTCATATATCTTTTGGCCACCATTTATATTCATGCAAGGTTTCAAGTAAAAAAG 585
DB 241 CTTTCTTCATATATCTTTTGGCCACCATTTATATTCATGCAAGGTTTCAAGTAAAAAAG 300

QY 586 AAGCAGTTTTCCGCAATTTGTTGACTATATGCTTTTTTGGTGTGTTGGGACTATTATT 645
DB 301 AAGCAGTTTTCCGCAATTTGTTGACTATATGCTTTTTTGGTGTGTTGGGACTATTATT 360

QY 646 TCTTGACAATCATATCTCTAGGTGTAACACAGATTTCTTTAAGAGTTTGGACATTGGAACC 705

Db 361 TCTTGACAATCATATCTCTAGGTGTAACACAGATTTCTTTAAGAGTTTGGACATTGGAACC 420
QY 706 TTTGACCTTGGGTGATTATCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 765
DB 421 TTTGACCTTGGGTGATTATCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 480
QY 766 AACTGCAAGTTCTGAATCAAGAGGACACCTTTGCTTTTACAGTCTTGTATTTCGGAGAG 825
DB 481 AACTGCAAGTTCTGAATCAAGAGGACACCTTTGCTTTTACAGTCTTGTATTTCGGAGAG 540
QY 826 GGTGTTGTTGAATGATGCAACGTCAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 885
DB 541 GGTGTTGTTGAATGATGCAACGTCAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 600
QY 886 ACTCACCTAAACCAACGAGCTGTTTTCATCTTCTTGGAAACTTCTTTGTTGTTGTTGTTGTT 945
DB 601 ACTCACCTAAACCAACGAGCTGTTTTCATCTTCTTGGAAACTTCTTTGTTGTTGTTGTTGTT 660
QY 946 CTAAGTACCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1005
DB 661 CTAAGTACCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 720
QY 1006 TACTTTGGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATGTTATGGCGTATCTT 1065
DB 721 TACTTTGGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATGTTATGGCGTATCTT 780
QY 1066 TCTTATATGCTGCTGAGCTTTTTCGACTTGAGCGGTATCTCTCACTGTGTTTCTGTGGT 1125
DB 781 TCTTATATGCTGCTGAGCTTTTTCGACTTGAGCGGTATCTCTCACTGTGTTTCTGTGGT 840
QY 1126 ATTGTGATGTCCCATTTACATATGSCACAATGTAAACGAGAGCTCAAGAAATACAAACAAG 1185
DB 841 ATTGTGATGTCCCATTTACATATGSCACAATGTAAACGAGAGCTCAAGAAATACAAACAAG 900
QY 1186 CATACCTTTGCAACTTTTGTCTATTTCTTTCGAGAGACATTTATTTTCTGTTGTTGGAATG 1245
DB 901 CATACCTTTGCAACTTTTGTCTATTTCTTTCGAGAGACATTTATTTTCTGTTGTTGGAATG 960
QY 1246 GATGCTTTGGACATTTGAACAAGTGGAGATCCGTTGAGTGACACACCGGGAACATCGATCGCA 1305
DB 961 GATGCTTTGGACATTTGAACAAGTGGAGATCCGTTGAGTGACACACCGGGAACATCGATCGCA 1020
QY 1306 GTGAGCTCAATCTTAATGGGTTCTGTCATGTTGTTGGAAGAGCAGGTTCTGTTTCCGTTA 1365
DB 1021 GTGAGCTCAATCTTAATGGGTTCTGTCATGTTGTTGGAAGAGCAGGTTCTGTTTCCGTTA 1080
QY 1366 TCGTTTCTATCTAACTTTAGCCAAAGAAATCAAAAGCGAGAAAATCAAATTTAAACATGCAG 1425
DB 1081 TCGTTTCTATCTAACTTTAGCCAAAGAAATCAAAAGCGAGAAAATCAAATTTAAACATGCAG 1140
QY 1426 GTTGTGATTTGGTGGTCTGTTCTCATGAGAGGTGCTGTATCTATGGTCTTTGTCATACAAC 1485
DB 1141 GTTGTGATTTGGTGGTCTGTTCTCATGAGAGGTGCTGTATCTATGGTCTTTGTCATACAAC 1200
QY 1486 AAGTTTCAAGGGCCGGGCAACAGATGTACGGGGGAATGCAATCATGATCAGCATCAGGATACG 1545
DB 1201 AAGTTTCAAGGGCCGGGCAACAGATGTACGGGGGAATGCAATCATGATCAGCATCAGGATACG 1260
QY 1546 ATAACTGTCTGTTCTTTTGTAGCACAGTGTGTTTGTGATGTCGACCAACCACTCATTAAGC 1605
DB 1261 ATAACTGTCTGTTCTTTTGTAGCACAGTGTGTTTGTGATGTCGACCAACCACTCATTAAGC 1320
QY 1606 TACATATTACCGCACCAAGAGCGCCACCGAGCATGTTATCTGTATGACACACACCCCAAAA 1665
DB 1321 TACATATTACCGCACCAAGAGCGCCACCGAGCATGTTATCTGTATGACACACACCCCAAAA 1380
QY 1666 TCCATATATATCCCTTTTGTGGACCAAGATCGTTTCAATGAGCCTTCAGGGAACCACAAT 1725
DB 1381 TCCATATATATCCCTTTTGTGGACCAAGATCGTTTCAATGAGCCTTCAGGGAACCACAAT 1440
QY 1726 GTGCTTCGGCTGACAGTATACGTGGCTTCTTGAACGGGCCACTCGAACCGTGCATTAC 1785
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Db 1441 GTGCTCGCCGACAGTATACGTGGCTTCTTGACACGCCCACTCGAACCCGTGCATTAC 1500
Qy 1786 TACTGAGACAATTTGATGACTCTTTCATGCGACCGCTTTGGAGGTCTGGCTTTGTA 1845
Db 1501 TACTGGAGACAATTTGATGACTCTTTCATGCGACCGCTTTGGAGGTCTGGCTTTGTA 1560
Qy 1846 CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAAACCTCTCTGATCTTTAGTAAGGCT 1899
Db 1561 CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAAACCTCTCTGATCTTTAGTAAGGCT 1614

RESULT 7
ADN11983
ID ADN11983 standard; DNA; 1563 BP.
XX
AC
XX
XX
ADN11983;
DT 17-JUN-2004 (first entry)
XX
DE AthNX1 mutant encoding sequence #2.
XX
KW salt tolerance; Na+/H+ transporter polypeptide; AtNHX1; ds.
XX
OS Synthetic.
XX
WO2004007668-A2.
XX
PN
XX
PD 22-JAN-2004.
XX
PF 09-JUL-2003; 2003WO-US021549.
XX
PR 12-JUL-2002; 2002US-0395662P.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Shi H, Blumwald E;
XX
DR WPI; 2004-122911/12.
XX
DR P-PSDB; ADN11984.
XX
PT Enhancing salt tolerance of a plant comprises introducing into the plant
PT a polynucleotide encoding a Na+/H+ transporter polypeptide.
XX
PS Claim 2; SEQ ID NO 5; 38pp; English.
XX
CC The present invention relates to enhancing salt tolerance of a plant
CC comprises introducing into the plant a polynucleotide encoding a Na+/H+
CC transporter polypeptide. The AtNHX1 gene confers salt tolerance. The
CC composition and methods are useful in conferring salt tolerance on plants
CC and other organisms. The present sequence represents a mutant AtNHX1
CC encoding sequence.
XX
SQ Sequence 1563 BP; 376 A; 333 C; 348 G; 506 T; 0 U; 0 Other;

Query Match : 71.8%; Score 1563; DB 12; Length 1563;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 286 ATGTGGATCTCTAGTTCGAAACTCGCTTGTATCGACATCTGATCAGCTTCTGTG 345
Db 1 ATGTGGATCTCTAGTTCGAAACTCGCTTGTATCGACATCTGATCAGCTTCTGTG 60

Qy 346 GTTGGTGAATCTCTTTGTTGCACCTCTTCTGCTGCTGATGTTCTTGGTCATCTTTG 405
Db 61 GTTGGTGAATCTCTTTGTTGCACCTCTTCTGCTGCTGATGTTCTTGGTCATCTTTG 120

Qy 406 GAAGAGATAGATGATGAACCAATCCATCACCGCTTGTGATTTGGGTAGGCACTGGT 465
Db 121 GAAGAGATAGATGATGAACCAATCCATCACCGCTTGTGATTTGGGTAGGCACTGGT 180

Qy 466 GTTACATTTGTTGATTAAGAAAAGCTCGCATCTTCTGCTTTAGTGAAGAT 525
Db 181 GTTACATTTGTTGATTAAGAAAAGCTCGCATCTTCTGCTTTAGTGAAGAT 240
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Qy 526 CTTTCTTTCATATATCTTTTGGCCACCCATATATTAATGAGGGTTTCAAGTAAAAAG 585
Db 241 CTTTCTTTCATATATCTTTTGGCCACCCATATATTAATGAGGGTTTCAAGTAAAAAG 300
Qy 586 AAGCAGTTTTTCCGCAATTTTCGTGACTATTAATGCTTTTGGTGTGTTGGGACTATTATT 645
Db 301 AAGCAGTTTTTCCGCAATTTTCGTGACTATTAATGCTTTTGGTGTGTTGGGACTATTATT 360
Qy 646 TCTTGCAAAATCATATCTCTAGGTGTACACAGTTCTTTAAGNAGTTGGACATTTGGAACC 705
Db 361 TCTTGCAAAATCATATCTCTAGGTGTAAACAGTTCTTTAAGNAGTTGGACATTTGGAACC 420
Qy 706 TTTGACTTTGGGTGATTATCTTTGCTATTGCTGCCATATTTGCTGCAACAGATTTCAGTATGT 765
Db 421 TTTGACTTTGGGTGATTATCTTTGCTATTGCTGCCATATTTGCTGCAACAGATTTCAGTATGT 480
Qy 766 ACATGTCAGGTTCTGAATCAAGACGAGACACCTTTGCTTTACAGTCTTTGATTCGAGAG 825
Db 481 ACATGTCAGGTTCTGAATCAAGACGAGACACCTTTGCTTTACAGTCTTTGATTCGAGAG 540
Qy 826 GGTGTTGTAATGATGCAACGTCAGTTGCTGCTTCAACGCGATTTCAGAGCTTTGATCTC 885
Db 541 GGTGTTGTAATGATGCAACGTCAGTTGCTGCTTCAACGCGATTTCAGAGCTTTGATCTC 600
Qy 886 ACTCACCTAAAACACGAGCTGCTTTTCATCTTTCTTGAAAACTTCTTGTATTTTGTCTC 945
Db 601 ACTCACCTAAAACACGAGCTGCTTTTCATCTTTCTTGAAAACTTCTTGTATTTTGTCTC 660
Qy 946 CTAAGTACCTTGTGTTGCTGCAACCGGTCGTAAAGTGCATGTTATCAAGAAGCTA 1005
Db 661 CTAAGTACCTTGTGTTGCTGCAACCGGTCGTAAAGTGCATGTTATCAAGAAGCTA 720
Qy 1006 TACTTTGGAAGGCACTCAACTGACGAGAGGTTGCCCTTATGATGCTTATGGCGTATCTT 1065
Db 721 TACTTTGGAAGGCACTCAACTGACGAGAGGTTGCCCTTATGATGCTTATGGCGTATCTT 780
Qy 1066 TCTTATATGCTTGTGAGCTTTTCGACTTTGAGCGGTATCTCTCAGTGTGTTTCTGTGGT 1125
Db 781 TCTTATATGCTTGTGAGCTTTTCGACTTTGAGCGGTATCTCTCAGTGTGTTTCTGTGGT 840
Qy 1126 ATTGATGATGCCCAATACATGACCAATGTAACGAGAGCTCAAGAATTAACAACAAG 1185
Db 841 ATTGATGATGCCCAATACATGACCAATGTAACGAGAGCTCAAGAATTAACAACAAG 900
Qy 1186 CATACCTTTGCAACTTTGTCATTTCTTCCGAGACATTTATTTCTTGTATGTTGGAATG 1245
Db 901 CATACCTTTGCAACTTTGTCATTTCTTCCGAGACATTTATTTCTTGTATGTTGGAATG 960
Qy 1246 GATGCTTTGACATTTGCAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1305
Db 961 GATGCTTTGACATTTGCAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1020
Qy 1306 GTGAGCTCAATCTTAATGGGTCTGCTCATGTTGTGGAAGAGAGCGTTCGTCTTTCCGTTA 1365
Db 1021 GTGAGCTCAATCTTAATGGGTCTGCTCATGTTGTGGAAGAGAGCGTTCGTCTTTCCGTTA 1080
Qy 1366 TCGTTTCTATCTAATTTAGCCCAAGNATCAAGCGGAAATCAACTTTAAACATGAG 1425
Db 1081 TCGTTTCTATCTAATTTAGCCCAAGNATCAAGCGGAAATCAACTTTAAACATGAG 1140
Qy 1426 GTTGTGATTTTGGTGTGCTGCTCATGAGAGGTGCTGATCTATGCTTCTTGGCTATGCAAC 1485
Db 1141 GTTGTGATTTTGGTGTGCTGCTCATGAGAGGTGCTGATCTATGCTTCTTGGCTATGCAAC 1200
Qy 1486 AAGTTTCAAGGGCGGGGACACAGATGTACCGGGAAATGCAATCATGATCACGATACG 1545
Db 1201 AAGTTTCAAGGGCGGGGACACAGATGTACCGGGAAATGCAATCATGATCACGATACG 1260
Qy 1546 ATAACTGCTGCTTTTGTAGCACAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1605
Db 1261 ATAACTGCTGCTTTTGTAGCACAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1320
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QY 1606 TACCTATTACCGCACCAGAACGCCACCGAGCATGTTATCTGATGACAAACACCCCAAAA 1665
Db |||||
QY 1321 TACCTATTACCGCACCAGAACGCCACCGAGCATGTTATCTGATGACAAACACCCCAAAA 1380
Db |||||
QY 1666 TCCATACATATCCCTTTGTTGGACCAAGACTCGTTTCATTGAGCCCTTCAGGGAACACCAAT 1725
Db |||||
QY 1381 TCCATACATATCCCTTTGTTGGACCAAGACTCGTTTCATTGAGCCCTTCAGGGAACCAAT 1440
QY 1726 GTGCTCGGCTGACAGTATAGTGGCTTCTTGACACGCGCCACTCGAAACCGTGCATTAC 1785
Db |||||
QY 1441 GTGCTCGGCTGACAGTATAGTGGCTTCTTGACACGCGCCACTCGAAACCGTGCATTAC 1500
QY 1786 TACTGGAGACAAATTTGATGACTCCCTTCATGCGACCGCTTTGGAGTCTGGCTTGTGTA 1845
Db |||||
QY 1501 TACTGGAGACAAATTTGATGACTCCCTTCATGCGACCGCTTTGGAGTCTGGCTTGTGTA 1560
QY 1846 CCC 1848
Db |||
QY 1561 CCC 1563

RESULT 8
ADN11989
ID ADN11989 standard; cDNA; 1566 BP.
XX
AC ADN11989;
XX
DT 17-JUN-2004 (first entry)
XX
DE NDL-1 encoding sequence.
XX
KW salt tolerance; Na+/H+ transporter polypeptide; AtNHX1; ss.
XX
OS Saccharomyces sp.
XX
PN WO2004007668-A2.
XX
PD 22-JAN-2004.
XX
PF 09-JUL-2003; 2003WO-US021549.
XX
PR 12-JUL-2002; 2002US-0395662P.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Shi H, Blumwald E;
XX
DR WPI; 2004-122911/12.
XX
P-PSDB; ADN11990.
XX
PT Enhancing salt tolerance of a plant comprises introducing into the plant
a polynucleotide encoding a Na+/H+ transporter polypeptide.
XX
PS Claim 2; SEQ ID NO 11; 38pp; English.
XX
CC The present invention relates to enhancing salt tolerance of a plant
comprises introducing into the plant a polynucleotide encoding a Na+/H+
transporter polypeptide. The AtNHX1 gene confers salt tolerance. The
composition and methods are useful in conferring salt tolerance on plants
and other organisms. The present sequence represents NDL-1 encoding
sequence.
XX
SQ Sequence 1566 BP; 378 A; 334 C; 349 G; 505 T; 0 U; 0 Other;

Query Match 71.8%; Score 1563; DB 12; Length 1566;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 337 GCTTCTGCTGGTTCGCTTGAATCTCTTTGTTGACACTCTTTGCTGCTGCTGCTGCTTGGT 396
Db |||||
QY 4 GCTTCTGCTGGTTCGCTTGAATCTCTTTGTTGACACTCTTTGCTGCTGCTGCTGCTTGGT 63
QY 397 CATCTTTTGGAGAGAAATAGATGGATGAACGAATCCATCACCGCTTTGTTGATTTGGGCTA 456
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Db |||||
QY 64 CATCTTTTGGAGAGAAATAGATGGATGAACGAATCCATCACCGCTTTGTTGATTTGGGCTA 123
QY 457 GGCACTGGTATTACCAATTTTGTGATTAGTAAGAAAGAAAGCTCGCATCTTCTCGTCTTT 516
Db |||||
QY 124 GGCACTGGTATTACCAATTTTGTGATTAGTAAGAAAGAAAGCTCGCATCTTCTCGTCTTT 183
QY 517 AGTGAAGATCTTTTCTCATATATCTTTTGGCCACCATTATATTCAATGCAAGGTTTCAA 576
Db |||||
QY 184 AGTGAAGATCTTTTCTCATATATCTTTTGGCCACCATTATATTCAATGCAAGGTTTCAA 243
QY 577 GTAAAAAAGACAGTCTTTTCCGCAATTTCTGCTACTATTATGCTTTTGGTCTGTTGGG 636
Db |||||
QY 244 GTAAAAAAGACAGTCTTTTCCGCAATTTCTGCTACTATTATGCTTTTGGTCTGTTGGG 303
QY 637 ACTATTATTTCTTGCACAATCATATCTCTAGGTGTAACACAGTCTTTTAAAGAAGTTGGAC 696
Db |||||
QY 304 ACTATTATTTCTTGCACAATCATATCTCTAGGTGTAACACAGTCTTTTAAAGAAGTTGGAC 363
QY 697 ATTGGAACCTTTGACTTGGGTGATTATCTTGCTATTGGTGCCATATTTGCTGCAACAGAT 756
Db |||||
QY 364 ATTGGAACCTTTGACTTGGGTGATTATCTTGCTATTGGTGCCATATTTGCTGCAACAGAT 423
QY 757 TCAGTATGTAACACTGACAGTCTTCTGAATCAAGACGAGACACCTTTGCTTTACAGTCTTGT 816
Db |||||
QY 424 TCAGTATGTAACACTGACAGTCTTCTGAATCAAGACGAGACACCTTTGCTTTACAGTCTTGT 483
QY 817 TTCGAGAGGGTGTGTAATGATGCAACGTCAGTCTGTTGTTCTTCAACGCGATTCAGAGC 876
Db |||||
QY 484 TTCGAGAGGGTGTGTAATGATGCAACGTCAGTCTGTTGTTCTTCAACGCGATTCAGAGC 543
QY 877 TTTGATCTCACTCACTTAAACCAAGAGCTCTTTTTCATCTTCTTGGAACTTCTTGTAT 936
Db |||||
QY 544 TTTGATCTCACTCACTTAAACCAAGAGCTCTTTTTCATCTTCTTGGAACTTCTTGTAT 603
QY 937 TTTGTTCTCTTAAGTACCTTGTGCTGCAACCGTCTGTAAGTGCCTATGTTATC 996
Db |||||
QY 604 TTTGTTCTCTTAAGTACCTTGTGCTGCAACCGTCTGTAAGTGCCTATGTTATC 663
QY 997 AAGAAGCTATATCTTTTGAAGGCACTCAACTGACGAGAGGTTGCCCTTATGATCTTATG 1056
Db |||||
QY 664 AAGAAGCTATATCTTTTGAAGGCACTCAACTGACGAGAGGTTGCCCTTATGATCTTATG 723
QY 1057 GCGTATCTTCTTATATGCTTGTGAGCTTTTTCAGCTTGTAGCGGTATCTTCACTGTGTTT 1116
Db |||||
QY 724 GCGTATCTTCTTATATGCTTGTGAGCTTTTTCAGCTTGTAGCGGTATCTTCACTGTGTTT 783
QY 1117 TTTCTGTGTATTGTGATGTCCCATTTACATGCGCACAAATGTAACGGAGAGCTCAAGAATA 1176
Db |||||
QY 784 TTTCTGTGTATTGTGATGTCCCATTTACATGCGCACAAATGTAACGGAGAGCTCAAGAATA 843
QY 1177 ACAACAAAGCATACCTTTTGCAACTTTTGTCAATTTCTTGGGAGACATTTATTTTCTTGTAT 1236
Db |||||
QY 844 ACAACAAAGCATACCTTTTGCAACTTTTGTCAATTTCTTGGGAGACATTTATTTTCTTGTAT 903
QY 1237 GTTGGAAATGATGCTTTGGCAATTTGCAATTTGAGTGGAGATCCGTGAGTGACACACCGGAC 1296
Db |||||
QY 904 GTTGGAAATGATGCTTTGGCAATTTGCAATTTGAGTGGAGATCCGTGAGTGACACACCGGAC 963
QY 1297 TCGATCCGAGTGAGCTCAATCTTAATGGGCTCTGCTCATGTTGGAAGAGAGCGTTCGTC 1356
Db |||||
QY 964 TCGATCCGAGTGAGCTCAATCTTAATGGGCTCTGCTCATGTTGGAAGAGAGCGTTCGTC 1023
QY 1357 TTTCCGTTATCGTTTCTTATCTTAAGTCCCAAGAAATCAAGCGAGAAATCAACTTTT 1416
Db |||||
QY 1024 TTTCCGTTATCGTTTCTTATCTTAAGTCCCAAGAAATCAAGCGAGAAATCAACTTTT 1083
QY 1417 AACATGCAAGTGTGATTTGGTGTCTGCTCTCATGAGAGTGTCTGTATCTATGGCTTT 1476
Db |||||
QY 1084 AACATGCAAGTGTGATTTGGTGTCTGCTCTCATGAGAGTGTCTGTATCTATGGCTTT 1143
QY 1477 GCATACAAAGTGTGATTTGCAAGGCGCGGACACACAGATGTAGCGGGAATGCAATCATGATC 1536
Db |||||
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Db 1144 GCATACAAAGTTTACAAAGGCGCGGCACACAGATGTACGCGGAATGCAATCATGATC 1203  
QY ACAGTACGATACGATGCTGCTTTTGTAGCACAGTGGTGTGTTGGTATGCTGACCAACCA 1596  
Db 1204 ACGAGTACGATACGATGCTGCTTTTGTAGCACAGTGGTGTGTTGGTATGCTGACCAACCA 1263  
QY TCATAAGTACGATACGATGCTGCTTTTGTAGCACAGTGGTGTGTTGGTATGCTGACCAAC 1656  
Db 1264 TCATAAGTACGATACGATGCTGCTTTTGTAGCACAGTGGTGTGTTGGTATGCTGACCAAC 1323  
QY ACCCCAAATCCATACATATCCCTTTGTGGACCAAGACTGCTTCATTTGAGCCTTCAGGG 1716  
Db 1324 ACCCCAAATCCATACATATCCCTTTGTGGACCAAGACTGCTTCATTTGAGCCTTCAGGG 1383  
QY 1717 AACCAATATGCTCGGCTGACAGTATACGCTGCTTCTTGACACGGCCCACTCGAAC 1776  
Db 1384 AACCAATATGCTCGGCTGACAGTATACGCTGCTTCTTGACACGGCCCACTCGAAC 1443  
QY GTGCATTAATCTAGTACGATCAATTTGATGATCTCTTTATGCGACCGCTTTTGGAGGTCGT 1836  
Db 1444 GTGCATTAATCTAGTACGATCAATTTGATGATCTCTTTATGCGACCGCTTTTGGAGGTCGT 1503  
QY 1837 GCTTTGTACCTTTGTTCCAGTTTCTCCAACTGAGAGAAACCTTCTGATCTTAGTAAG 1896  
Db 1504 GCTTTGTACCTTTGTTCCAGTTTCTCCAACTGAGAGAAACCTTCTGATCTTAGTAAG 1563  
QY 1897 GCT 1899  
Db 1564 GCT 1566

RESULT 9

ADN11985  
ID ADN11985 standard; DNA; 1473 BP.  
XX ADN11985;  
AC  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE AtNHX1 mutant encoding sequence #3.  
XX  
KW salt tolerance; Na+/H+ transporter polypeptide; AtNHX1; ds.  
XX  
OS Synthetic.  
XX  
PN WO2004007668-A2.  
XX  
PD 22-JAN-2004.  
XX  
PF 09-JUL-2003; 2003WO-US021549.  
XX  
PR 12-JUL-2002; 2002US-0395662P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Shi H, Blumwald E;  
XX  
DR WPI; 2004-122911/12.  
DR P-FSDB; ADN11986.  
XX  
PT Enhancing salt tolerance of a plant comprises introducing into the plant  
PT a polynucleotide encoding a Na+/H+ transporter polypeptide.  
XX  
PS Claim 4; SEQ ID NO 7; 38pp; English.  
XX  
CC The present invention relates to enhancing salt tolerance of a plant  
CC comprises introducing into the plant a polynucleotide encoding a Na+/H+  
CC transporter polypeptide. The AtNHX1 gene confers salt tolerance. The  
CC composition and methods are useful in conferring salt tolerance on plants  
CC and other organisms. The present sequence represents a mutant AtNHX1  
CC encoding sequence.  
XX  
SQ Sequence 1473 BP; 358 A; 306 C; 327 G; 482 T; 0 U; 0 Other;

Query Match  
Best Local Similarity 67.6%; Score 1473; DB 12; Length 1473;  
Matches 1473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 286 ATGTTGGATCTCTAGTGTGCAAACTGCTGCTTATCGACATCTGATCAGCCTTCTGTG 345  
Db 1 ATGTTGGATCTCTAGTGTGCAAACTGCTGCTTATCGACATCTGATCAGCCTTCTGTG 60  
QY GTTGGTTGAATCTCTTTGTTGCACTTCTTTGTGCTGCTTATTTGTTCTTGGTCACTTTTG 405  
Db 61 GTTGGTTGAATCTCTTTGTTGCACTTCTTTGTGCTGCTTATTTGTTCTTGGTCACTTTTG 120  
QY 406 GAAGAGATAGATGATGATGCAATCCATCACCGCTTTGTTGATTTGGGCTAGGCACTGCT 465  
Db 121 GAAGAGATAGATGATGATGCAATCCATCACCGCTTTGTTGATTTGGGCTAGGCACTGCT 180  
QY 466 GTTACCATTGTTGATTTAGTAAAGGAAAAAGCTGCGATCTTCTGCTCTTTAGTGAAGAT 525  
Db 181 GTTACCATTGTTGATTTAGTAAAGGAAAAAGCTGCGATCTTCTGCTCTTTAGTGAAGAT 240  
QY 526 CTTTCTTTCATATATCTTTGCGCACTTATTTCAATGCAAGGCTTTCAAGTAAAG 585  
Db 241 CTTTCTTTCATATATCTTTGCGCACTTATTTCAATGCAAGGCTTTCAAGTAAAG 300  
QY 586 AAGCAGTTTTCGCAATCTCTGCTGCTTATTTGCTGCTGCTTGGGCACTTATTT 645  
Db 301 AAGCAGTTTTCGCAATCTCTGCTGCTTATTTGCTGCTGCTTGGGCACTTATTT 360  
QY 646 TCTTGCACAATCATATCTCTAGGTGTAACAGATTTCTTAAAGAGTTCGACATTTGGAACC 705  
Db 361 TCTTGCACAATCATATCTCTAGGTGTAACAGATTTCTTAAAGAGTTCGACATTTGGAACC 420  
QY 706 TTTGACTTGGGTGATTTATCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 765  
Db 421 TTTGACTTGGGTGATTTATCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
QY 766 ACACCTGCAAGTTCGAAATCAAGACGAGACACCTTTTGTCTTTACAGTCTTTGTTCCGAGAG 825  
Db 481 ACACCTGCAAGTTCGAAATCAAGACGAGACACCTTTTGTCTTTACAGTCTTTGTTCCGAGAG 540  
QY 826 GGTGTTGGAATGATGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 885  
Db 541 GGTGTTGGAATGATGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
QY 886 ACTCACCTAAACACGAGCTGCTTTTCATCTTCTTGGAACTTCTGCTGCTGCTGCTGCTGCT 945  
Db 601 ACTCACCTAAACACGAGCTGCTTTTCATCTTCTTGGAACTTCTGCTGCTGCTGCTGCTGCT 660  
QY 946 CTAAGTACCTTTGCTTGGTGTGCAACCGGTCTGATTAAGTGGGTATGTTATCAAGAAAGCTA 1005  
Db 661 CTAAGTACCTTTGCTTGGTGTGCAACCGGTCTGATTAAGTGGGTATGTTATCAAGAAAGCTA 720  
QY 1006 TACTTTGGAAGGCACTCAACTGACGAGAGTTCCTTATGATGCTTATGGCGTATCTT 1065  
Db 721 TACTTTGGAAGGCACTCAACTGACGAGAGTTCCTTATGATGCTTATGGCGTATCTT 780  
QY 1066 TCTTATATGCTTGTGAGCTTTTTCGACTTGTAGCGGTATCTTCTGCTGCTGCTGCTGCTGCT 1125  
Db 781 TCTTATATGCTTGTGAGCTTTTTCGACTTGTAGCGGTATCTTCTGCTGCTGCTGCTGCTGCT 840  
QY 1126 ATTGTGATGTCCTTATACATGCAATGTAACGAGAGCTCAAGAAATCAACAAAG 1185  
Db 841 ATTGTGATGTCCTTATACATGCAATGTAACGAGAGCTCAAGAAATCAACAAAG 900  
QY 1186 CATACCTTTGCAACTTTGTCATTTCTTGGGAGACATTTATTTCTTGTATGTTGGAATG 1245  
Db 901 CATACCTTTGCAACTTTGTCATTTCTTGGGAGACATTTATTTCTTGTATGTTGGAATG 960  
QY 1246 GATGCTTTGGACATTTGACAACTGAGATCCGCTGAGTGCACACCGGGGACATCGATCGCA 1305  
Db 961 GATGCTTTGGACATTTGACAACTGAGATCCGCTGAGTGCACACCGGGGACATCGATCGCA 1020



QY 1306 GTGAGCTCAATCCCTAATGGGCTCGTCATGCTGGAGAGCAGCGTTCGCTTCCGTTA 1365  
Db |||||  
QY 1021 GTGAGCTCAATCCCTAATGGGCTCGTCATGCTGGAGAGCAGCGTTCGCTTCCGTTA 1080  
Db |||||  
QY 1366 TCGTTCTCTATCTAACTTAGCCAAAGAAATCAAAAGCGAGAAAATCAACTTTAAACATGCAG 1425  
Db TCGTTCTCTATCTAACTTAGCCAAAGAAATCAAAAGCGAGAAAATCAACTTTAAACATGCAG 1140  
QY 1426 GTTGATGTTGGTGTCTGGTCTCATGAGAGGTGCTGTATCTATGGCTTTGGCATACAAC 1485  
Db GTTGATGTTGGTGTCTGGTCTCATGAGAGGTGCTGTATCTATGGCTTTGGCATACAAC 1200  
QY 1486 AAGTTTACAAGGGCGGGCACACAGATGTCGCGGAATGCAATCATGATCAACAGTACG 1545  
Db |||||  
QY 1201 AAGTTTACAAGGGCGGGCACACAGATGTCGCGGAATGCAATCATGATCAACAGTACG 1260  
QY 1546 ATAACTGTCTCTTTTATAGCACAGTGGTGTGGTATGCTGACCAACCACTCATAGC 1605  
Db ATAACTGTCTCTTTTATAGCACAGTGGTGTGGTATGCTGACCAACCACTCATAGC 1320  
QY 1606 TACCTATTACCGACACAGAACGCCACACAGAGCATGTTATCTGATGACAAACCCCAAAA 1665  
Db TACCTATTACCGACACAGAACGCCACACAGAGCATGTTATCTGATGACAAACCCCAAAA 1380  
QY 1666 TCCATACATATCCCTTTGTTGGACCAAGACTCGTTCTATGGACCTTCAGGGAACCAAT 1725  
Db |||||  
QY 1381 TCCATACATATCCCTTTGTTGGACCAAGACTCGTTCTATGGACCTTCAGGGAACCAAT 1440  
QY 1726 GTGGCTCGGCTGACAGTATACGTGGCTTCTTG 1758  
Db GTGGCTCGGCTGACAGTATACGTGGCTTCTTG 1473

## RESULT 10

ADN11991

ID ADN11991 standard; cDNA; 1410 BP.

XX

AC ADN11991;

XX

DT 17-JUN-2004 (first entry)

XX

DE NDL-2 encoding sequence.

XX

KW salt tolerance; Na<sup>+</sup>/H<sup>+</sup> transporter polypeptide; AtNHX1; ss.

XX

OS *Saccharomyces* sp.

XX

PN WO2004007668-A2.

XX

PD 22-JAN-2004.

XX

PP 09-JUL-2003; 2003WO-US021549.

XX

PR 12-JUL-2002; 2002US-0395662P.

XX

PA (REGC ) UNIV CALIFORNIA.

XX

PI Shi H, Blumwald E;

XX

DR WPI; 2004-122911/12.

XX

DP P-PSDB; ADN11992.

XX

XX Enhancing salt tolerance of a plant comprises introducing into the plant

PT a polynucleotide encoding a Na<sup>+</sup>/H<sup>+</sup> transporter polypeptide.

XX

PS Claim 4; SEQ ID NO 13; 38pb; English.

XX

XX The present invention relates to enhancing salt tolerance of a plant

CC comprises introducing into the plant a polynucleotide encoding a Na<sup>+</sup>/H<sup>+</sup>

CC transporter polypeptide. The AtNHX1 gene confers salt tolerance. The

CC composition and methods are useful in conferring salt tolerance on plants

CC and other organisms. The present sequence represents NDL-2 encoding

CC sequence.

CC

XX SQ Sequence 1410 BP; 348 A; 309 C; 309 G; 444 T; 0 U; 0 Other;  
Query Match 64.6%; Score 1407; DB 12; Length 1410;  
Best Local Similarity 100.0%; Pred. No. 6.7e-308;  
Matches 1407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 493 AAAAGCTCGCATCTTCTCGTCTTTAGTGAAGATCTTTCTTCATATATCTTTGGCCACCC 552  
Db |||||  
QY 553 ATTATATTCAATGAGGTTTCAAGTAAAAAAGACAGTTTTTCCGCAATTTCTGCTACT 612  
Db ATTATATTCAATGAGGTTTCAAGTAAAAAAGACAGTTTTTCCGCAATTTCTGCTACT 123  
QY 613 ATTATGCTTTTGGTGTCTGGGACTATTATTCTTGGCACAATCATATCTCTAGGTGTA 672  
Db ATTATGCTTTTGGTGTCTGGGACTATTATTCTTGGCACAATCATATCTCTAGGTGTA 183  
QY 673 ACACAGTCTTTAAGAAGTTGGACATTTGGAACCTTTTGACTTGGTGATTAATCTTCTATT 732  
Db ACACAGTCTTTAAGAAGTTGGACATTTGGAACCTTTTGACTTGGTGATTAATCTTCTATT 243  
QY 733 GGTGCCATATTGCTGCAACAGATTCAATGATGTACACTGCAGGTTCTGAATCAAGACGAG 792  
Db GGTGCCATATTGCTGCAACAGATTCAATGATGTACACTGCAGGTTCTGAATCAAGACGAG 303  
QY 793 ACACCTTTGCTTACAGTCTTGTATTCGGAGAGGTTGTGAATGATGCAACGCTAGTT 852  
Db ACACCTTTGCTTACAGTCTTGTATTCGGAGAGGTTGTGAATGATGCAACGCTAGTT 363  
QY 853 GTGGTCTTCAACGGGATTGAGCTTTGATCTCACTCACTTAACCAAGAGCTGCTTTT 912  
Db GTGGTCTTCAACGGGATTGAGCTTTGATCTCACTCACTTAACCAAGAGCTGCTTTT 423  
QY 913 CATCTCTTGGAAACTTCTTGTATTCTTCTAAGTACCTTGTCTGGTCTGCAACC 972  
Db CATCTCTTGGAAACTTCTTGTATTCTTCTAAGTACCTTGTCTGGTCTGCAACC 483  
QY 973 GGTCTGATAAGTGGTATGTTATCAAGAAGCTATCTTTTGGAGGCACTCAACTGACCGA 1032  
Db GGTCTGATAAGTGGTATGTTATCAAGAAGCTATCTTTTGGAGGCACTCAACTGACCGA 543  
QY 1033 GAGGTTGCCCTTATGATGCTTATGGCGTATCTTCTTATATGCTTGTGAGCTTTTCGAC 1092  
Db GAGGTTGCCCTTATGATGCTTATGGCGTATCTTCTTATATGCTTGTGAGCTTTTCGAC 603  
QY 1093 TTGAGCGGTATCCTCACTGTGTTTTTCTGTGGTATTGTGATGTCCCATTAACATGGCAC 1152  
Db TTGAGCGGTATCCTCACTGTGTTTTTCTGTGGTATTGTGATGTCCCATTAACATGGCAC 663  
QY 1153 AATGTAAACGAGAGCTCAAGAAATCAACAAAGACATACCTTTTGAACCTTTGTCTATTCTT 1212  
Db AATGTAAACGAGAGCTCAAGAAATCAACAAAGACATACCTTTTGAACCTTTGTCTATTCTT 723  
QY 1213 GCGGAGACATTTATTTTCTTGTATGTTGGATGGATGCTTGGACATTTGCAAGTGGAGA 1272  
Db GCGGAGACATTTATTTTCTTGTATGTTGGATGGATGCTTGGACATTTGCAAGTGGAGA 783  
QY 1273 TCCGTGAGTGCACACACCGGAAACATCCATCGCAGTGAGCTCAATCTTAATGGGTCTGGTC 1332  
Db TCCGTGAGTGCACACACCGGAAACATCCATCGCAGTGAGCTCAATCTTAATGGGTCTGGTC 843  
QY 1333 ATGTTTGAAGAGAGCGGTTTCGCTTTTCGTTATTCGTTTCTATCTTAACCTTAGCAAGAAG 1392  
Db ATGTTTGAAGAGAGCGGTTTCGCTTTTCGTTATTCGTTTCTATCTTAACCTTAGCAAGAAG 903  
QY 1393 AATCAAGCGGAGAAATCAACATGCAAGTTGATTTGGTGTCTGCTCATG 1452  
Db AATCAAGCGGAGAAATCAACATGCAAGTTGATTTGGTGTCTGCTCATG 963  
QY 1453 AGAGGTCTCTATCTATGGCTCTTGGCATACAACAAAGTTTACAAGGGCGGGCACACAGAT 1512  
Db |||||

Db 964 AGAGTGTGTATATCTTGTGCATACAAAGTTTTCAAGGGCGGGCACAGAT 1023  
QY 1513 GTACGGGGAATGCAATCATGATCAGAGTACGATAACTGTCTGCTTTTATAGCACAGTG 1572  
Db 1024 GTACGGGGAATGCAATCATGATCAGAGTACGATAACTGTCTGCTTTTATAGCACAGTG 1083  
QY 1573 GTGTTTGGTATGCTGACCAAAACACTCATAAGCTACCTATTACCGCACCAAGCCACC 1632  
Db 1084 GTGTTTGGTATGCTGACCAAAACACTCATAAGCTACCTATTACCGCACCAAGCCACC 1143  
QY 1633 ACAGCATCTTATCTGTAGTACACACACCCCAAAATCCATACATATCCCTTTGTGGACCA 1692  
Db 1144 ACAGCATCTTATCTGTAGTACACACACCCCAAAATCCATACATATCCCTTTGTGGACCA 1203  
QY 1693 GACTCGTTCATTTAGAGCTTTGAGGAACACCAATGTGCGCTCGGCTGACAGTATACGTGGC 1752  
Db 1204 GACTCGTTCATTTAGAGCTTTGAGGAACACCAATGTGCGCTCGGCTGACAGTATACGTGGC 1263  
QY 1753 TTCTTGACACGGCCCACTCGAACCGTGCAATTAATCTACTGGAGACAAATTTGATGACTCCTTC 1812  
Db 1264 TTCTTGACACGGCCCACTCGAACCGTGCAATTAATCTACTGGAGACAAATTTGATGACTCCTTC 1323  
QY 1813 ATGCGACCGCTTTGGAGGTGCTGGCTTTGTACCCCTTTGTTCCAGGTTCTCCAACTGAG 1872  
Db 1324 ATGCGACCGCTTTGGAGGTGCTGGCTTTGTACCCCTTTGTTCCAGGTTCTCCAACTGAG 1383  
QY 1873 AGAAACCCCTCGTATCTTAGTAAGGCT 1899  
Db 1384 AGAAACCCCTCGTATCTTAGTAAGGCT 1410

RESULT 11  
ADN11987  
ID ADN11987 standard; DNA; 1362 BP.  
XX  
AC ADN11987;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE AtNHX1 mutant encoding sequence #4.  
XX  
KW salt tolerance; Na+/H+ transporter polypeptide; AtNHX1; ds.  
XX  
OS Synthetic.  
XX  
PN WO2004007668-A2.  
XX  
PD 22-JAN-2004.  
XX  
PF 09-JUL-2003; 2003WO-US021549.  
XX  
PR 12-JUL-2002; 2002US-0395662P.  
XX  
PA (REGC) UNIV CALIFORNIA.  
XX  
PI Shi H, Blumwald E;  
XX  
DR WPI: 2004-122911/12.  
DR P-PSDB; ADN11988.  
XX  
PT Enhancing salt tolerance of a plant comprises introducing into the plant  
PT a polynucleotide encoding a Na+/H+ transporter polypeptide.  
PS Claim 7; SEQ ID NO 9; 38pp; English.  
XX  
CC The present invention relates to enhancing salt tolerance of a plant  
CC comprises introducing into the plant a polynucleotide encoding a Na+/H+  
CC transporter polypeptide. The AtNHX1 gene confers salt tolerance. The  
CC composition and methods are useful in conferring salt tolerance on plants  
CC and other organisms. The present sequence represents a mutant AtNHX1  
XX encoding sequence.  
SQ Sequence 1362 BP; 329 A; 274 C; 305 G; 454 T; 0 U; 0 Other;

Query Match  
Best Local Similarity 62.5%; Score 1362; DB 12; Length 1362;  
Matches 1362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 286 ATGTTGGATCTCTAGTGTGAAACTGCTTCTGTTATCGACATCTGATCAGCTTCTGTG 345  
Db 1 ATGTTGGATCTCTAGTGTGAAACTGCTTCTGTTATCGACATCTGATCAGCTTCTGTG 60  
QY 346 GTTGGTTGAATCTCTTGTGCACTTCTTGTGCTGTTATGTTCTTGGTCACTTTTG 405  
Db 61 GTTGGTTGAATCTCTTGTGCACTTCTTGTGCTGTTATGTTCTTGGTCACTTTTG 120  
QY 406 GAAGAGATAGATGGATGAACGAATCCATCACCGCTTGTGTTGATGGGCTAGGCACTGT 465  
Db 121 GAAGAGATAGATGGATGAACGAATCCATCACCGCTTGTGTTGATGGGCTAGGCACTGT 180  
QY 466 GTTACCATTTTGTGATTAAGTAAAGGAAAAAGCTGCACTCTTCTGTTCTTTAGTGAAGAT 525  
Db 181 GTTACCATTTTGTGATTAAGTAAAGGAAAAAGCTGCACTCTTCTGTTCTTTAGTGAAGAT 240  
QY 526 CTTTCTTCATATATCTTTTGGCCACCCATTAATCAATGCAAGGTTTCAAGTAAAAAAG 585  
Db 241 CTTTCTTCATATATCTTTTGGCCACCCATTAATCAATGCAAGGTTTCAAGTAAAAAAG 300  
QY 586 AAGCAGTTTTTCCGCAATTTCTGCTGACTATTAATGCTTTTGGTCTGTTGGGACTATTATT 645  
Db 301 AAGCAGTTTTTCCGCAATTTCTGCTGACTATTAATGCTTTTGGTCTGTTGGGACTATTATT 360  
QY 646 TCTTGCACAATCATATCTCTAGGTGTAAACAGAGTTCTTTAAAGAGTTTGGACATTCGAACC 705  
Db 361 TCTTGCACAATCATATCTCTAGGTGTAAACAGAGTTCTTTAAAGAGTTTGGACATTCGAACC 420  
QY 706 TTTGACTTGGGTGATTATCTGCTATTTGGTGCCATATTTGCTGCAACAGATTCAGTATGT 765  
Db 421 TTTGACTTGGGTGATTATCTGCTATTTGGTGCCATATTTGCTGCAACAGATTCAGTATGT 480  
QY 766 ACCTGCAAGTTCCTGAATCAAGACGAGACACCTTTGCTTTACAGTCTTGTATTCGGAGAG 825  
Db 481 ACCTGCAAGTTCCTGAATCAAGACGAGACACCTTTGCTTTACAGTCTTGTATTCGGAGAG 540  
QY 826 GGTGTTGGAATGATGCAACCTGATGTTGCTTCAACGCGATTCAGAGCTTTGATCTC 885  
Db 541 GGTGTTGGAATGATGCAACCTGATGTTGCTTCAACGCGATTCAGAGCTTTGATCTC 600  
QY 886 ACTCACCTAAACCGAGAGCTGCTTTTCATCTTCTGGAACCTTCTGATTTGTTTCTC 945  
Db 601 ACTCACCTAAACCGAGAGCTGCTTTTCATCTTCTGGAACCTTCTGATTTGTTTCTC 660  
QY 946 CTAAGTACCTTGTGTTGGTGTGCAACCGGTCTGATAAGTGGGTATGTTATCAAGAAAGCTA 1005  
Db 661 CTAAGTACCTTGTGTTGGTGTGCAACCGGTCTGATAAGTGGGTATGTTATCAAGAAAGCTA 720  
QY 1006 TACTTTGGAAGGCACTCAACTGACCGAGAGTTGCCCTTATGATGCTTTATGGCGTATCTT 1065  
Db 721 TACTTTGGAAGGCACTCAACTGACCGAGAGTTGCCCTTATGATGCTTTATGGCGTATCTT 780  
QY 1066 TCTTATATGCTTGTGAGCTTTTTCGACTTGGAGCGGTATCTCTGCTGTTTCTGCTGCT 1125  
Db 781 TCTTATATGCTTGTGAGCTTTTTCGACTTGGAGCGGTATCTCTGCTGTTTCTGCTGCT 840  
QY 1126 ATTGTGATGTCCTCCATTAACATGCAATGCAATGTAACGGAGAGCTCAAGAAATCAACAAG 1185  
Db 841 ATTGTGATGTCCTCCATTAACATGCAATGTAACGGAGAGCTCAAGAAATCAACAAG 900  
QY 1186 CATACCTTTGCAACTTGTGCAATTTCTTGGGAGACATTTATTTCTTGTATGTTGGAAATG 1245  
Db 901 CATACCTTTGCAACTTGTGCAATTTCTTGGGAGACATTTATTTCTTGTATGTTGGAAATG 960  
QY 1246 GATGCTTTGGACATTTGACAGTGGAGATCCGTGAGTGAACACCGGGAGACATCGATCGCA 1305  
Db 961 GATGCTTTGGACATTTGACAGTGGAGATCCGTGAGTGAACACCGGGAGACATCGATCGCA 1020

QY 1306 GTGAGCTCAATCCTAATGGGTCTGGTTCATGGTTGGAAGAGCAGCGTTCGTCTTTCCGTTA 1365  
Db |||||  
QY 1021 GTGAGCTCAATCCTAATGGGTCTGGTTCATGGTTGGAAGAGCAGCGTTCGTCTTTCCGTTA 1080  
Db |||||  
QY 1366 TCGTTTCTATCTAATCTTACCCAAAGAAATCAAAGCGAGAAATCAAATTTAAACATGCAG 1425  
Db |||||  
QY 1081 TCGTTTCTATCTAATCTTACCCAAAGAAATCAAAGCGAGAAATCAAATTTAAACATGCAG 1140  
Db |||||  
QY 1426 GTTGTGATTTGGTGTCTGGTCTCATGAGAGGTGCTGTATCTATGGCTCTTGCATACAAC 1485  
Db |||||  
QY 1141 GTTGTGATTTGGTGTCTGGTCTCATGAGAGGTGCTGTATCTATGGCTCTTGCATACAAC 1200  
Db |||||  
QY 1486 AAGTTTACAAGGCGCGGCACACAGATGTACGCGGAATGCAATCATGATCACAGTAGC 1545  
Db |||||  
QY 1201 AAGTTTACAAGGCGCGGCACACAGATGTACGCGGAATGCAATCATGATCACAGTAGC 1260  
Db |||||  
QY 1546 ATAACGTCTGTCTTTTATAGCACAGTGTGTTGGTATGCTGACCAACCACTCATAGC 1605  
Db |||||  
QY 1261 ATAACGTCTGTCTTTTATAGCACAGTGTGTTGGTATGCTGACCAACCACTCATAGC 1320  
Db |||||  
QY 1606 TACCTATTACCGCACAGAACGCCACACGAGCATGTTATCT 1647  
Db |||||  
QY 1321 TACCTATTACCGCACAGAACGCCACGAGCATGTTATCT 1362  
Db |||||

RESULT 12

ADN11993  
ID ADN11993 standard; cDNA; 1323 BP.

XX AC ADN11993;

XX DT 17-JUN-2004 (first entry)

XX DE NDL-3 encoding sequence.

XX KW salt tolerante; Na+/H+ transporter polypeptide; AtNHX1; ss.

XX OS Saccharomyces sp.

XX PN WO2004007668-A2.

XX PD 22-JAN-2004.

XX PF 09-JUL-2003; 2003WO-US021549.

XX PR 12-JUL-2002; 2002US-0395662P.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Shi H, Blumwald E;

XX DR WPI; 2004-122911/12.

XX DR P-PSDB; ADN11994.

PT Enhancing salt tolerance of a plant comprises introducing into the plant a polynucleotide encoding a Na+/H+ transporter polypeptide.

PS Claim 7; SEQ ID NO 15; 38pp; English.

XX The present invention relates to enhancing salt tolerance of a plant comprises introducing into the plant a polynucleotide encoding a Na+/H+ transporter polypeptide. The AtNHX1 gene confers salt tolerance. The composition and methods are useful in conferring salt tolerance on plants and other organisms. The present sequence represents NDL-3 encoding sequence.

SQ Sequence 1323 BP; 326 A; 290 C; 297 G; 410 T; 0 U; 0 Other;

Query Match 60.6%; Score 1320.4; DB 12; Length 1323;

Best Local Similarity 99.9%; Pred. No. 2.5e-288; Matches 1321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 578 TAAAAAAGAAGCAGTTTTTCGCAATTTTCGTACTATTATGCTTTTGGTGTGTGGGA 637

Db |||||  
QY 2 TGA AAAAGAGCAGTTTTTCGCAATTTTCGTACTATTATGCTTTTGGTGTGTGGGA 61  
QY 638 CTATTTATTTCTTGCAAAATCATATCTCTAGGTGTAAACACAGTTCTTTAAGAGTTGACA 697  
Db |||||  
QY 62 CTATTTATTTCTTGCAAAATCATATCTCTAGGTGTAAACACAGTTCTTTAAGAGTTGACA 121  
QY 698 TTGGAACCTTTGACCTTCGGGTGATTTATCTTGTCTATTTGGTGCATATTTGCTGCAACAGATT 757  
Db |||||  
QY 122 TTGGAACCTTTGACCTTCGGGTGATTTATCTTGTCTATTTGGTGCATATTTGCTGCAACAGATT 181  
QY 758 CAGTATGTACACTGCAGGTTCTGAATCAAGACGAGACACCTTTGCTTTTACAGTCTTTGAT 817  
Db |||||  
QY 182 CAGTATGTACACTGCAGGTTCTGAATCAAGACGAGACACCTTTGCTTTTACAGTCTTTGAT 241  
QY 818 TCGAGAGGGTGTGTGAATGATGCAACCGTTCAGTTGGTCTTCAACGCGATTCAGAGCT 877  
Db |||||  
QY 242 TCGAGAGGGTGTGTGAATGATGCAACCGTTCAGTTGGTCTTCAACGCGATTCAGAGCT 301  
QY 878 TTGATCTCACTCACTTAAACCAACGAGCTGCTTTTTCATCTTCTTGGAAACTTCTTGTATT 937  
Db |||||  
QY 302 TTGATCTCACTCACTTAAACCAACGAGCTGCTTTTTCATCTTCTTGGAAACTTCTTGTATT 361  
QY 938 TGTCTCTCTAAAGTACCTTGTCTGCTGCTCAACCGGTCTGATAAGTGCCTTATGATCA 997  
Db |||||  
QY 362 TGTCTCTCTAAAGTACCTTGTCTGCTGCTCAACCGGTCTGATAAGTGCCTTATGATCA 421  
QY 998 AGAAGCTATATCTTTGGAAGGCACTCAACGACGAGAGGTTGCCCTTATGATGTTATGG 1057  
Db |||||  
QY 422 AGAAGCTATATCTTTGGAAGGCACTCAACGACGAGAGGTTGCCCTTATGATGTTATGG 481  
QY 1058 CGTATCTTTCTTATATGCTTGTGAGCTTTTCGACTTTGAGCGGTATCTCTCACTGTGTTT 1117  
Db |||||  
QY 482 CGTATCTTTCTTATATGCTTGTGAGCTTTTCGACTTTGAGCGGTATCTCTCACTGTGTTT 541  
QY 1118 TCTGTGTATTTGTGATGTCCTTATACACATGGCAATTAACGAGAGAGCTCAAGAATAA 1177  
Db |||||  
QY 542 TCTGTGTATTTGTGATGTCCTTATACACATGGCAATTAACGAGAGAGCTCAAGAATAA 601  
QY 1178 CAACAAAGCATACCTTTGCAACTTTTGTTCATTTCTTGGGAGACATTTATTTCTTGTATG 1237  
Db |||||  
QY 602 CAACAAAGCATACCTTTGCAACTTTTGTTCATTTCTTGGGAGACATTTATTTCTTGTATG 661  
QY 1238 TTGGAATGGAATGCTTGGACATTTGACAAAGTGGAGATCCGTGAGTGACACACCGGGAACAT 1297  
Db |||||  
QY 662 TTGGAATGGAATGCTTGGACATTTGACAAAGTGGAGATCCGTGAGTGACACACCGGGAACAT 721  
QY 1298 CGATCGCAGTGAGCTCAATCCTAATGGGTCTGTGTCATGGTTGGAGAGCAGCTTCGTCT 1357  
Db |||||  
QY 722 CGATCGCAGTGAGCTCAATCCTAATGGGTCTGTGTCATGGTTGGAGAGCAGCTTCGTCT 781  
QY 1358 TTCGTTATCGTTTCTATCTAACTTTAGCCAAGAAATCAAAAGCGAGAAATCAACTTTA 1417  
Db |||||  
QY 782 TTCGTTATCGTTTCTATCTAACTTTAGCCAAGAAATCAAAAGCGAGAAATCAACTTTA 841  
QY 1418 ACATGCAAGTTGATGATTTGGTGTCTGTCTCATGAGAGGTCGTGATCTATGCTCTTG 1477  
Db |||||  
QY 842 ACATGCAAGTTGATGATTTGGTGTCTGTCTCATGAGAGGTCGTGATCTATGCTCTTG 901  
QY 1478 CATACAACAAGTTTACAAAGGCGCGGCACACAGATGTACGCGGAATGCAATCATGATCA 1537  
Db |||||  
QY 902 CATACAACAAGTTTACAAAGGCGCGGCACACAGATGTACGCGGAATGCAATCATGATCA 961  
QY 1538 CGAGTAGATAAATCTGTCTGTCTTTTATAGCACAGTGGTGTGGTGTGATGCTGACCAACAC 1597  
Db |||||  
QY 962 CGAGTAGATAAATCTGTCTGTCTTTTATAGCACAGTGGTGTGGTGTGATGCTGACCAACAC 1021  
QY 1598 TCATAAGCTACCTATTACCGCACAGAACCGCACAGAGATGTTATCTGATGACAAACA 1657  
Db |||||  
QY 1022 TCATAAGCTACCTATTACCGCACAGAACCGCACAGAGATGTTATCTGATGACAAACA 1081  
QY 1658 CCCCCAAATCCATACATATCCCTTTTGTGGACCAAGACTCGTTCATTTGAGCCTTCAGGA 1717  
Db |||||

Db 1082 CCCAAATCCATACATATCCCTTTGTTGGACAAGACTCGTTCAATGAGCCCTTCAGGGA 1141  
Qy 1718 ACCAATGTGCTCGGCTGACAGTATACGTGGCTTCTTGACACGGCCCACTCGAACCG 1777  
Db 1142 ACCAATGTGCTCGGCTGACAGTATACGTGGCTTCTTGACACGGCCCACTCGAACCG 1201  
Qy 1778 TGCATTACTGAGACAAATTTGATGATCTCTTCATGCGACCCGCTTTTGGAGGTCGTG 1837  
Db 1202 TGCATTACTGAGACAAATTTGATGATCTCTTCATGCGACCCGCTTTTGGAGGTCGTG 1261  
Qy 1838 GCTTTGCTACCTTTGTTCCAGGTTCTCCAACTGAGAGAACCTCTCTGATCTTAGTAGG 1897  
Db 1262 GCTTTGCTACCTTTGTTCCAGGTTCTCCAACTGAGAGAACCTCTCTGATCTTAGTAGG 1321  
Qy 1898 CT 1899  
Db 1322 CT 1323  
RESULT 13  
ADM68265  
ID ADM68265 standard; DNA; 1449 BP.  
XX  
AC ADM68265;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Plant Na+/H+ antiporter protein gene.  
XX  
DE ds; gene; salt-resistance; MGX4; mangrove; drought-resistance; plant;  
KW transgenic plant; Na+/H+ antiporter protein; NHX1.  
KW Unidentified.  
XX  
OS CN1448511-A.  
XX  
PI 15-OCT-2003.  
XX  
PF 02-APR-2002; 2002CN-00111229.  
XX  
PR 02-APR-2002; 2002CN-00111229.  
XX  
PA (ZHAN/) ZHANG H.  
XX  
PI Zhang H;  
XX  
DR WPI; 2004-091822/10.  
XX  
PT Salt tolerance gene MGX4 and method of breeding a salt and drought  
PT tolerant plant variety.  
XX  
PS Disclosure; Page 10-12; 19pp; Chinese.  
XX  
CC The invention relates to a novel salt-resistance gene MGX4 from mangrove  
CC or other drought-resistant plant. Breeding a salt and drought resistant  
CC plant variety comprises fusing the gene with the forced constitutive  
CC expression promoter 35S to generate vector pHXZ. The gene is transfected  
CC into a recipient plant by agrobacterium mediated transfection to give a  
CC salt and drought tolerant transgenic plant. This sequence corresponds to  
CC the DNA encoding a plant MGX4 protein. The sequence is used for  
CC comparison with the Arabidopsis thaliana NHX1 gene.  
XX  
SQ Sequence 1449 BP; 355 A; 326 C; 304 G; 464 T; 0 U; 0 Other;  
Query Match 38.9%; Score 848; DB 12; Length 1449;  
Best Local Similarity 82.0%; Pred. No. 1.6e-181;  
Matches 977; Conservative 0; Mismatches 215; Indels 0; Gaps 0;  
Qy 427 GAATCCATCACCCTGTTGATTGGCTAGGCACTGGTGTACCAATTTGTTGATTAGT 486  
Db 198 GATTTCATCACCCTGTTGATTGGCTAGGCACTGGTGTACCAATTTGTTGATTAGT 257  
Qy 487 AAAGGAAAAAGCTCGCATCTTCTCGTCTTTTAGTGAAGATCTTTTCTCATATATCTTTG 546

Db 258 AAAGGAAAAAGCTCGCATCTTCTCGTCTTTAGTGAAGATCTTTTCTCATATATCTTTG 317  
Qy 547 CCACCCATTATATTCAAATGCAGGGTTTCAAGTAAAAAAGACAGCTTTTCCGCAATTC 606  
Db 318 CCACCCATTATATTCAAATGCAGGGTTTCAAGTAAAAAAGACAGCTTTTCCGCAATTC 377  
Qy 607 GTGACTATATGCTTTTGGTGTCTGTGGGACTATTTATTTCTTGACAAATCATATCTCTA 666  
Db 378 GTGACTATATGCTTTTGGTGTCTGTGGGACTATTTATTTCTTGACAAATCATATCTCTA 437  
Qy 667 GGTGTAAACACAGTCTTTTAAAGATTGACATTTGAACTTTTGACTTGGGTGATTATCTT 726  
Db 438 GGTGTAAACACAGTCTTTTAAAGATTGACATTTGAACTTTTGACTTGGGTGATTATCTT 497  
Qy 727 GCTATTGCTGCCATATTTGCTGCACAGATTCAGTATGTACACTGCAGGTTCTGAAATCAA 786  
Db 498 GCTATTGCTGCCATATTTGCTGCACAGATTCAGTATGTACACTGCAGGTTCTGAAATCAA 557  
Qy 787 GACGAGACACCTTTGCTTTTACAGTCTTGTATTTCCGAGAGGGTGTGTGAATGATCAACG 846  
Db 558 GACGAGACACCTTTGCTTTTACAGTCTTGTATTTCCGAGAGGGTGTGTGAATGATCAACG 617  
Qy 847 TCAGTTGTGCTTCAACGCGATTTCAGAGCTTTGATCTCCTCACTCACTAAACCAACGAGCT 906  
Db 618 TCAGTTGTGCTTCAACGCGATTTCAGAGCTTTGATCTCCTCACTCACTAAACCAACGAGCT 677  
Qy 907 GCTTTTCATCTCTTGGAACTTCTTGTATTTTCTTCTTAAGTACCTTGTCTGGTGTCT 966  
Db 678 GCTTTTCATCTCTTGGAACTTCTTGTATTTTCTTCTTAAGTACCTTGTCTGGTGTCT 737  
Qy 967 GCAACCGCTGTGATAAGTGCCTGTATGTATCAAGAGCTATATCTTGGAGGCACTCAACT 1026  
Db 738 GCAACCGCTGTGATAAGTGCCTGTATGTATCAAGAGCTATATCTTGGAGGCACTCAACT 797  
Qy 1027 GACGAGAGGTTGCCCTTATGATGCTTATGCGTATCTTTCTTATATCTTGTCTGAGCTT 1086  
Db 798 GACGAGAGGTTGCCCTTATGATGCTTATGCGTATCTTTCTTATATCTTGTCTGAGCTT 857  
Qy 1087 TTCGACTTGGGGTATCTCTCACTGTGTTTTCTGTGGTATGTGATCTCCCATTTACACA 1146  
Db 858 TTCGACTTGGGGTATCTCTCACTGTGTTTTCTGTGGTATGTGATCTTCACTTACTCC 917  
Qy 1147 TGGCAATGTAAACGAGAGCTCAAGATAACAAACAAAGACTACCTTTGCAACTTTGTCA 1206  
Db 918 TGGCATCAAGTGACAGAAGGATTTAAGTTACCAACAGCAATTCATTTGTAATCTTAGGA 977  
Qy 1207 TTTCTTGGGAGACATTTATTTTCTTGTATGTTTGAATGGAATGCGCTTGGACATTCACAAG 1266  
Db 978 TTCATTATCGAACTATTCTCTGGCTCTATGTTAAACATGGATATATTGGACCTAGAGAC 1037  
Qy 1267 TGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCAGTGAGCTCAATCTTAATGGGT 1326  
Db 1038 TGGAGATTAGCTAGCTAGAGTCTTAAGAGACCAATTTCTGTAACGCAATTTATTTTGACA 1097  
Qy 1327 CTGCTCATGTTTGAAGAGCAGCGTTCTGCTTTTCGTTATCGTTTCTATCTAACTTAGCC 1386  
Db 1098 TTGGTTATGATTGGAAGAGTCGATTTATATTCCTTTGAAATTTCCGATCCACCTACAA 1157  
Qy 1387 AAGAAGAAATCAACGAGAGAAATCAACTTTTAAACATGCAAGTTGTGATTTGGTGTCTGGT 1446  
Db 1158 AAAGGGACGCGGATCCAAAGAAATCAACTTCGAAACACAACTAACTTATGTTGCTAGT 1217  
Qy 1447 CTCATGAGAGGTGCTGATCTATGCTCTTGCATACAAACAGTTTACAGGCCCGGGCAC 1506  
Db 1218 CTCATGAGAGGCAATTTTCAGTTGCGGTTCTTTTATACCAAGTTTAAACGCACTGGTCCAC 1277  
Qy 1507 ACAGATGTACCGGGAATGCAATCATGATCACGAGTACGATAACTGTCTGCTTTTTAGC 1566  
Db 1278 TCTGAATCCGACTCAATGTATCATGTTAACCAGCACTTATTTGTTATTTCTATTCGGC 1337  
Qy 1567 ACAGTGTGTTTGGTATGCTGACCAACCACTATAAGCTACCTATTAACCGC 1618

Db 1338 ACAATGGCTTTCACACTGGTGACGCGCGGTAGCAAGTATCTCTCTCCAC 1389

RESULT 14  
AAA72926  
ID AAA72926 standard; DNA; 1668 BP.  
XX  
AC AAA72926;  
XX  
XX 06-AUG-2003 (revised)  
DT 23-NOV-2000 (first entry)  
XX  
XX  
DE Atlixplex gmelini Na<sup>+</sup> and H<sup>+</sup> antiporter protein encoding DNA.  
XX  
XX  
KW Atlixplex gmelini; Na plus and H plus antiporter protein;  
KW Na<sup>+</sup> and H<sup>+</sup> antiporter protein; transformed plant; high salt tolerance;  
ds.  
XX  
XX  
OS Atlixplex gmelini.  
XX  
PN JP2000157287-A.  
XX  
XX 13-JUN-2000.  
XX  
XX 16-SEP-1999; 99JP-00261606.  
XX  
XX 24-SEP-1998; 98JP-00269504.  
XX  
XX (SHOK-) SHOKUBUTSU KOGAKU KK.  
XX  
XX WPI: 2000-468209/41.  
DR P-PSDB; AAB12786.  
XX  
XX An Na<sup>+</sup> and H<sup>+</sup> plus antiporter protein and a gene encoding it.  
PT  
PS Claim 1; Page 9-10; 16pp; Japanese.  
XX  
XX The present sequence encodes an Na<sup>+</sup> and H<sup>+</sup> antiporter protein isolated  
CC from Atlixplex gmelini. The Na<sup>+</sup> and H<sup>+</sup> antiporter protein and gene  
CC encoding it are useful for the preparation of transformed plants with  
CC high salt tolerance, e.g. for growth in arid land. (Updated on 06-AUG-  
CC 2003 to correct OS field.)  
XX  
SQ Sequence 1668 BP; 397 A; 342 C; 376 G; 553 T; 0 U; 0 Other;

Query Match 38.2%; Score 832.8; DB 3; Length 1668;  
Best Local Similarity 71.9%; Pred. No. 4.5e-178;  
Matches 1146; Conservative 0; Mismatches 412; Indels 36; Gaps 3;

QY 323 CGACATCTGATCACGCTTCTGGTGGTGGTGAATCTCTTTGTCACCTCTTTGGTGT 382  
Db 50 CCACCTCTGATCACGCTTCTGGTGGTGGTGGTGAATCTCTTTGTCACCTCTTTGGTGT 109

QY 383 GTATTGTTCTTGGTCACTCTTTTGGAGAGATAGATGGATGAACCAATCCATCACCGCT 442  
Db 110 GTATCGTAATTGGTCACTCTCTAGAGAGATCGTTGGATGAATGAGTCCATCTGCCC 169

QY 443 TGTGATTGGGTAGGCACTGGTGTACCAATTTGTTGATTAGTAAAGAAAAGCTGCG 502  
Db 170 TTCTTATAGGTTTGGCTACTGGGTTGTGATCTCTGCTATTAGTGGAGAAAAGTTCA 229

QY 503 ATCTTCTGCTTTAGTGAAGATCTTTCTCATATATCTTTTGGCCACCCATTAATTC 562  
Db 230 ATCTTTTGGTCTTCAGTGAAGATCTTTCTCATATATCTTTTCCCGATTATATTC 289

QY 563 ATGCAAGGTTTCAAGTAAAGAAAGACAGTCTTTTCCGCAATTTCTGACTATTATGCTTT 622  
Db 290 ATGCAAGGTTTCAAGTGAAGAGAGACAGTCTTTCCGCAATTTCTGACTATTATGTT 349

QY 623 TTGGTGTCTTGGGACTATATTTCTTGTGCAAAATCATATCTCTAGGTGTAAACAGTTCT 682  
Db 350 TTGGAGCTGTGGTACTATGGTATCAATTCACCATCATATCTCTGGGAGCGTTGTCAAATTT 409

QY 683 TTAAGAGTGTGGACATTTGGAACTTTGACTTGGGTGATTAATCTTGTCTATTGTTGTCATAT 742  
Db 410 TTAAGAAATTTGGATTTGGTACTCTGGAGTTGGCAGACTATCTTGCATTTGGTGAATAT 469

QY 743 TTGCTGCAACAGATTTCAGTATGTACACTGCAAGTTTCTGAATCAAGACGAGACACTTTGC 802  
Db 470 TCGTGCACACAGATTCTGTTTGGCAGACTGCACTGCAAGTTCTTAATCAGGATGAGACCCCTCTGC 529

QY 803 TTTACAGTCTTGTATTCGGAGAGGGTGTGTGAATGATGCAACCTGCTAGTTGTGTCTTCA 862  
Db 530 TCTACAGTCTGGTCTTTGGCGAGGGTGTGTGAATGATGCAACCTGCTAGTTGTGTCTTCA 589

QY 863 ACGGATTCAGAGCTTTGATCTCACTCACTAAACACGAGCTGCTTTTTCATCTCTTG 922  
Db 590 ATGCAATTCAGAGCTTTGACCTCAAGAAATTTGATACAGATAGCTTTTACATTTATGG 649

QY 923 GAAACTCTCTGTTATTTGTTCTCCTAAAGTACTTTGCTTGGTGTGCTGCAACCGGTCTGATA 982  
Db 650 GCAACTTCTTATTTTATTCGCAAGCAGTACTTTGGAGCAATTTACTTGGCTTGCTCA 709

QY 983 GTGCTATGTATCAAGAGCTATCTTTGGAAGGCACTCAACTGACCGAGAGGTTGCC 1042  
Db 710 GTGCTTACATTTATCAAAAAGCTGTACTTTGGAAGGCAATTTCCACTGATCTGAGGTTGCTT 769

QY 1043 TTATGATGCTTATGCGGTATCTTTCTTATATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 1102  
Db 770 TAATGATGCTTATGCTTATCTTATCTTACATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 829

QY 1103 TCCTCAGTGTGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1162  
Db 830 TTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 889

QY 1163 AGACTCAAGATTAACAAAGCACTACTTTGCAACTTTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1222  
Db 890 AGAGCTCAAGAGTAAACCAAGCATGCTTTTGAACATCTATCTTTTGTGCTGAGGTTT 949

QY 1223 TTTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1282  
Db 950 TCCTATTTCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1009

QY 1283 ACACACCGGGAACATCGATCGAGTGAATCAATCTTAATGGGCTGCTGCTGCTGCTGCTGCTGCT 1342  
Db 1010 ATAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1069

QY 1343 GAGCAGGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1402  
Db 1070 GAGCAGGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1129

QY 1403 AGAAATCAACTTTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1462  
Db 1130 AAAAGGTCACTTTTCAACGAGCAATTTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1189

QY 1463 TATCTATGGCTTCTTGCATCAACAAAGTTTACAAGGCGCGGCAACACAGATGTACCGCGGA 1522  
Db 1190 TTTCCATGGCACTTTGCTTATAATCAGTTTACAGGCTCTGGGCAACACAGCTTAGGGGAA 1249

QY 1523 ATGCAATCATGATCAAGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1582  
Db 1250 ATGCAATCATGATCAAGCACTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1309

QY 1583 TGCTGACCAACCACTCATAGCTACCTATTTACCGCACCAAGACCGCACCAAC-----GA 1636  
Db 1310 TGCTGACCAACCACTCATAGCTACCTATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1369

QY 1637 GCATGTTATCTGATGACCAACCCCAAAAT-----CC 1668  
Db 1370 GCACCGTATCAGATGTGGGAAGTCCAAAGTCATACTCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1429

QY 1669 ATACATATCCCTTTGTTGGACCAAGATCTGTTTCAATGAGCTTTCAGGGAAACAC--AATG 1726  
Db 1430 AAGATTATGAAGTTGATGTGGGAAACCGAAACCAATGAAGACACCACTGAGCGCGGAGCTA 1489

QY 1727 TGCCTCGGCTGACAGTATACGTGGCTTCTTGACACGCGCCCACTCGAACCCTGCTGCTGCTGCTGCT 1786



Db	1803	ACTGTTGTCCTTTTTCAGCACAGTGGTATTTGGGTTGATGACAAACCTTTAAATTCATTATTA	1862
Qy	1606	TACCTATTACCGCACCAAGCGCCACACAGAGCATGTTATCTGATGACAAACCCCAAAA	1665
Db	1863	TTGTTACCTCACA AAAACATTGATCAGAAATGATCTCCTCTGAAACGATGATCTCCAAA	1922
Qy	1666	TCCATACATATCCCTTTTGTGGACCAAGACTCGTTTCATTGAGCCTTCAGGGAAACCACAAT	1725
Db	1923	TCCTTCATTGTGCCACTTCTTTGACAGCACACAAGACTCAGAAGCTGATCTGGCGCGACAT	1982
Qy	1726	GTGCCTCGGCTGCAGTATACGTGGCTTCTTGACAGCGGCCACTCGAAACGGTGCATTAC	1785
Db	1983	GTACCCCGTCCCCACAGTTTGC GGATGCTCCTGTCAACCCCATCTCACGGTACATTAC	2042
Qy	1786	TACTGGAGACAAATTTGATGACTCCCTTCATGCGACCGCTCTTTGGAGGTCTGTGGCTTTGTA	1845
Db	2043	TACTGGAGAAAATTTGACATGCATTCATGGCTCTGTTTTCGGTGGACGAGGTTTTGTA	2102
Qy	1846	CCCTTTGTTCCAGGTCTCCAACTGA	1871
Db	2103	CCTTTGTGTTCCAGGATCACTTACTGA	2128

Search completed: August 28, 2005, 02:57:21  
Job time : 1191 secs





Qy	61	AGCTTCAA	AAATTTTG	AATTTTGA	CTCTTGGG	CTCTTTTG	TAAATCAG	ACTGAA	GATAT	120
Db	61	AGCTTCAA	AAATTTTG	AATTTTGA	CTCTTGGG	CTCTTTTG	TAAATCAG	ACTGAA	GATAT	120
Qy	121	TTAGATTACC	CAGAGTTGT	TCAAGGAATGG	TTTCAGTGC	GACGACGGA	AGATAA	AAG	180	
Db	121	TTAGATTACC	CAGAGTTGT	TCAAGGAATGG	TTTCAGTGC	GACGACGGA	AGATAA	AAG	180	
Qy	181	AGACTTTTTT	TCAGATTTTG	CTGATCCAAA	ATCTGAATAG	TGTGTTCA	TGTTCTTG	GGAT	240	
Db	181	AGACTTTTTT	TCAGATTTTG	CTGATCCAAA	ATCTGAATAG	TGTGTTCA	TGTTCTTG	GGAT	240	
Qy	241	CAAACTCG	GAAGAGG	AAGTTTGT	TGGATCTAG	AAGAAGATA	CAAAATGTT	GGATCTCT	300	
Db	241	CAAACTCG	GAAGAGG	AAGTTTGT	TGGATCTAG	AAGAAGATA	CAAAATGTT	GGATCTCT	300	
Qy	301	GTGTCG	AAACCTG	CTTGGT	TATCGACA	ATCTGATC	ACGCTTCTG	TGTTGGAATCTC	360	
Db	301	GTGTCG	AAACCTG	CTTGGT	TATCGACA	ATCTGATC	ACGCTTCTG	TGTTGGAATCTC	360	
Qy	361	TTTCTG	TCACTCTT	CTTGCTG	TGTTATTTG	TCTTGGT	TCATCTTTT	TGGAAGAGAATAG	420	
Db	361	TTTCTG	TCACTCTT	CTTGCTG	TGTTATTTG	TCTTGGT	TCATCTTTT	TGGAAGAGAATAG	420	
Qy	421	ATGAAC	GAATCC	ATCACG	CGCTTG	TGATTGGG	CTAGGC	ACTGGTGTAC	480	
Db	421	ATGAAC	GAATCC	ATCACG	CGCTTG	TGATTGGG	CTAGGC	ACTGGTGTAC	480	
Qy	481	ATTAGT	AAAGG	AAAGCTG	CGATCTTCT	CGTCTTTAG	TAGGAAG	ATCTTTTCTCAT	540	
Db	481	ATTAGT	AAAGG	AAAGCTG	CGATCTTCT	CGTCTTTAG	TAGGAAG	ATCTTTTCTCAT	540	
Qy	541	CTTTTGC	CACTTAT	TATTAAT	CAATG	CAGGGTTTCA	AGTAAAG	AAGACGAGTTTTC	600	
Db	541	CTTTTGC	CACTTAT	TATTAAT	CAATG	CAGGGTTTCA	AGTAAAG	AAGACGAGTTTTC	600	
Qy	601	AAATTCG	TGACTA	TATATG	CTTTTTT	TGGTCTGTTGGG	ACTATATTT	CTTGCA	CAATCAT	660
Db	601	AAATTCG	TGACTA	TATATG	CTTTTTT	TGGTCTGTTGGG	ACTATATTT	CTTGCA	CAATCAT	660
Qy	661	TCTCTAG	TGTAA	CACAGT	TCTTTA	GAAAGTTG	GACAATG	GAACTTTGA	CTTGGG	720
Db	661	TCTCTAG	TGTAA	CACAGT	TCTTTA	GAAAGTTG	GACAATG	GAACTTTGA	CTTGGG	720
Qy	721	TATCTT	CGTAT	TGTTG	CGCATATTT	CTGCAAC	AGATTCAG	TATGAC	CTGCAGGTTCTG	780
Db	721	TATCTT	CGTAT	TGTTG	CGCATATTT	CTGCAAC	AGATTCAG	TATGAC	CTGCAGGTTCTG	780
Qy	781	AATCA	GACG	AGAC	ACCTTTG	CTTTAC	AGTCTTGTAT	TCGAG	AGGGTGTGTG	840
Db	781	AATCA	GACG	AGAC	ACCTTTG	CTTTAC	AGTCTTGTAT	TCGAG	AGGGTGTGTG	840
Qy	841	GCAACG	TAGTTGG	TCTTCA	ACGGAATC	AGAGCTTTG	ATCTCACT	CACTAA	ACCAC	900
Db	841	GCAACG	TAGTTGG	TCTTCA	ACGGAATC	AGAGCTTTG	ATCTCACT	CACTAA	ACCAC	900
Qy	901	GAAGCTG	CTTTTCA	CTCTT	CTGGAA	CTTCTTGT	TATTTGTTCT	CTCTA	AGTACCTTGCTT	960
Db	901	GAAGCTG	CTTTTCA	CTCTT	CTGGAA	CTTCTTGT	TATTTGTTCT	CTCTA	AGTACCTTGCTT	960
Qy	961	GGTCTG	CAACCG	GTCTG	ATAAGT	CGCTATG	TATCAAGA	AGCTATAT	ACTTTGGA	1020
Db	961	GGTCTG	CAACCG	GTCTG	ATAAGT	CGCTATG	TATCAAGA	AGCTATAT	ACTTTGGA	1020
Qy	1021	TCAA	CTGAC	CGAG	AGTTG	CCCTTAT	GATGCTT	ATAG	CGGTATCTTTCT	1080
Db	1021	TCAA	CTGAC	CGAG	AGTTG	CCCTTAT	GATGCTT	ATAG	CGGTATCTTTCT	1080
Qy	1081	GAGCTTTT	TCGACTT	GAGGGT	ATCCTCA	CTGTGTTTTT	CTGTG	TATG	TGATGATGCC	1140
Db	1081	GAGCTTTT	TCGACTT	GAGGGT	ATCCTCA	CTGTGTTTTT	CTGTG	TATG	TGATGATGCC	1140
Qy	1141	TACACAT	GGCA	CAATGT	AAACG	GAGGCTCA	AGAAATA	CAACAA	AGCATAC	1200

1141	Db	 TACACATGGCACAATGTAAACGGAGAGCTCAAGAATAACAAACAAGCATACCTTTGGCACT	1200
1201	Qy	TTGTCTATTTCTTCGGGAGACATTTATTTTCTTGATGTGTTGGAATGATGCTTTGGACATT	1260
1201	Db	TTGTCTATTTCTTCGGGAGACATTTATTTTCTTGATGTGTTGGAATGATGCTTTGGACATT	1260
1261	Qy	GACAAAGTGGAGATCCCGTGTGATGACACACCGGGAAACATCGATCGCAGTGAAGCTCAATCCCTA	1320
1261	Db	GACAAAGTGGAGATCCCGTGTGATGACACACCGGGAAACATCGATCGCAGTGAAGCTCAATCCCTA	1320
1321	Qy	ATGGGTCTGGTCATGGTTTGGAAAGAGAGCGTTCGTCTTTCCGTTATCGTTTCTATCTTAAC	1380
1321	Db	ATGGGTCTGGTCATGGTTTGGAAAGAGAGCGTTCGTCTTTCCGTTATCGTTTCTATCTTAAC	1380
1381	Qy	TTTAGCCAAAGAAGAAATCAAAAGCGAGAAATCAACTTTTAAACATGCAGGTCTGTGATTTGCTGG	1440
1381	Db	TTTAGCCAAAGAAGAAATCAAAAGCGAGAAATCAACTTTTAAACATGCAGGTCTGTGATTTGCTGG	1440
1441	Qy	TCCTGGTCTCATGAGAGGTGCTGTATCTATGGCTCTTTGCATACAACAAGTTTACAAGGGCC	1500
1441	Db	TCCTGGTCTCATGAGAGGTGCTGTATCTATGGCTCTTTGCATACAACAAGTTTACAAGGGCC	1500
1501	Qy	GGGACACACAGATGTACCGGGAAATGCAATCATGATCACAGGTACGATACTGTCTGTCTTT	1560
1501	Db	GGGACACACAGATGTACCGGGAAATGCAATCATGATCACAGGTACGATACTGTCTGTCTTT	1560
1561	Qy	TTTAGCACACAGTGGTGTGTTGGTATGCTGACCAAAACCACTCATTAAGCTTACCTATTACCGCAC	1620
1561	Db	TTTAGCACACAGTGGTGTGTTGGTATGCTGACCAAAACCACTCATTAAGCTTACCTATTACCGCAC	1620
1621	Qy	CAGAACGCCACACGAGCATGTTTATCTGATGACAAACCCCAAAATPCCATACATATCCCT	1680
1621	Db	CAGAACGCCACACGAGCATGTTTATCTGATGACAAACCCCAAAATPCCATACATATCCCT	1680
1681	Qy	TTGTTGGACCAAGACTCGTTTATTTGAGCCTTCAGGGAAACCAATGTGTGCTCGGCTGAC	1740
1681	Db	TTGTTGGACCAAGACTCGTTTATTTGAGCCTTCAGGGAAACCAATGTGTGCTCGGCTGAC	1740
1741	Qy	AGTATACGTGGCTTCTTGACACGGCCCACTCGAAACCGTGCATTCATCTACCTGGAGACAATTT	1800
1741	Db	AGTATACGTGGCTTCTTGACACGGCCCACTCGAAACCGTGCATTCATCTACCTGGAGACAATTT	1800
1801	Qy	GATGACTCTCTTCATGCGACCCGCTTTTGGAGTCTGTGGCTTTGTACCCCTTTGTCAGGT	1860
1801	Db	GATGACTCTCTTCATGCGACCCGCTTTTGGAGTCTGTGGCTTTGTACCCCTTTGTCAGGT	1860
1861	Qy	TCCTCCAACTGAGAGAACCTCTCTGATCTTAGTAAGCTTGAGGGTAAACGTGGAGAAA	1920
1861	Db	TCCTCCAACTGAGAGAACCTCTCTGATCTTAGTAAGCTTGAGGGTAAACGTGGAGAAA	1920
1921	Qy	GCTTTGATTTTTTTTGGTAGAAAAGGTGATTCAAATTTATGCTTTTGTGTAAATTTATCCA	1980
1921	Db	GCTTTGATTTTTTTTGGTAGAAAAGGTGATTCAAATTTATGCTTTTGTGTAAATTTATCCA	1980
1981	Qy	TTTGTAATATPTGTTGTGAGGACAGAAAATCTGCTTAAACGTTTTGTAGAGAGAGAACAAA	2040
1981	Db	TTTGTAATATPTGTTGTGAGGACAGAAAATCTGCTTAAACGTTTTGTAGAGAGAGAACAAA	2040
2041	Qy	ACATGGCAACTTTGAAGTGTTCATTTGATGATGTAATATATATTCATATTTGTTTTGTTG	2100
2041	Db	ACATGGCAACTTTGAAGTGTTCATTTGATGATGTAATATATATTCATATTTGTTTTGTTG	2100
2101	Qy	TAACACAAACTACACATTTGTTTTATGTTTTGTAATTTGGTTTTTGTCTCGAAAAA	2160
2101	Db	TAACACAAACTACACATTTGTTTTATGTTTTGTAATTTGGTTTTTGTCTCGAAAAA	2160
2161	Qy	AAAAAAAAAAAAAAAAAAAA 2178	
2161	Db	AAAAAAAAAAAAAAAAAAAA 2178	

US-10-617-624-1  
; Sequence 1, Application US/10617624  
; Publication No: US20050034191A1  
; GENERAL INFORMATION:  
; APPLICANT: Blumwald, Eduardo  
; TITLE OF INVENTION: SALT TOLERANT OIL CROPS  
; FILE REFERENCE: 529642000500  
; CURRENT APPLICATION NUMBER: US/10/617,624  
; CURRENT FILING DATE: 2003-07-10  
; PRIOR APPLICATION NUMBER: US 60/395,656  
; PRIOR FILING DATE: 2002-07-12  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2178  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-10-617-624-1

Query Match 100.0%; Score 2178; DB 21; Length 2178;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CTCTCTGTTTCTCTCTGTCAGCAAGAAAGAAATCTCAGGTTTACGTTTTCGA	60
DB	1	CTCTCTGTTTCTCTCTGTCAGCAAGAAAGAAATCTCAGGTTTACGTTTTCGA	60
QY	61	AGCTTCCAAATTTTCAATTTTTCATCTCTGGGCTCTTTTGTAAATCAGACTGAGATAT	120
DB	61	AGCTTCCAAATTTTCAATTTTTCATCTCTGGGCTCTTTTGTAAATCAGACTGAGATAT	120
QY	121	TTAGATTACCCAGAAGTGTTCAGGAATGTTTCAGTGGACAGACGGAAGATAAAG	180
DB	121	TTAGATTACCCAGAAGTGTTCAGGAATGTTTCAGTGGACAGACGGAAGATAAAG	180
QY	181	AGACTTTTTCAGATTTTGTCTGATCCAAATCTGAATAGTTTCAATGTTTGGAT	240
DB	181	AGACTTTTTCAGATTTTGTCTGATCCAAATCTGAATAGTTTCAATGTTTGGAT	240
QY	241	CAAAATCGGAAGAGAGAGTGTTCGATCTAGCAAGATCAATGTTTGGATCTCTA	300
DB	241	CAAAATCGGAAGAGAGAGTGTTCGATCTAGCAAGATCAATGTTTGGATCTCTA	300
QY	301	GTGTGAAATCGCTTCGTTATCGACATCTGATCAGCTTCTGTGTTGGTTCGATCTC	360
DB	301	GTGTGAAATCGCTTCGTTATCGACATCTGATCAGCTTCTGTGTTGGTTCGATCTC	360
QY	361	TTTGTGTCATCTTTTGTGTTGATGTTTCTTGGTCACTTTTGGAGAGATAGATGG	420
DB	361	TTTGTGTCATCTTTTGTGTTGATGTTTCTTGGTCACTTTTGGAGAGATAGATGG	420
QY	421	ATGAAGGAATCCATACCGCTTGTGATTTGGCTAGGCACTGGTGTACCAATTTTGTG	480
DB	421	ATGAAGGAATCCATACCGCTTGTGATTTGGCTAGGCACTGGTGTACCAATTTTGTG	480
QY	481	ATTAGTAAAGGAAAAAGCTCGCATCTCTCGTCTTTAGTGAAGATCTTTTTCATATAT	540
DB	481	ATTAGTAAAGGAAAAAGCTCGCATCTCTCGTCTTTAGTGAAGATCTTTTTCATATAT	540
QY	541	CTTTTCCCAACCCATTTATTTCAATGACGGTTTCAAGTAAAAAAGAACGAGTTTTTCCGC	600
DB	541	CTTTTCCCAACCCATTTATTTCAATGACGGTTTCAAGTAAAAAAGAACGAGTTTTTCCGC	600
QY	601	AATTTGCTGACTATTATGCTTTTGTGCTGTTGGGACTATTATTCTTGGCAATCATAT	660
DB	601	AATTTGCTGACTATTATGCTTTTGTGCTGTTGGGACTATTATTCTTGGCAATCATAT	660
QY	661	TCCTAGGTTAAACAGATCTTTTAAAGAGTTGGACATTTGGAACTTTGACTTGGGTGAT	720
DB	661	TCCTAGGTTAAACAGATCTTTTAAAGAGTTGGACATTTGGAACTTTGACTTGGGTGAT	720
QY	721	TATCTTGTCTATTTGGTCCCATATTTGCTGCAACAGATTTCAGTATGTACCTGACGTTCTG	780
DB	721	TATCTTGTCTATTTGGTCCCATATTTGCTGCAACAGATTTCAGTATGTACCTGACGTTCTG	780

DB	721	TATCTTGTCTATTTGGTCCCATATTTGCTGCAACAGATTTCAGTATGTACCTGACGTTCTG	780
QY	781	AATCAAGACGAGACACCTTTGCTTTTACAGTCTTTGTTATTCGAGAGAGGTTGTTGTAATGAT	840
DB	781	AATCAAGACGAGACACCTTTGCTTTTACAGTCTTTGTTATTCGAGAGAGGTTGTTGTAATGAT	840
QY	841	GCAACGTGAGTTTGTGTTCTTCAACCGGATTCAGAGCTTTGATCTCACTCACCTAAACAC	900
DB	841	GCAACGTGAGTTTGTGTTCTTCAACCGGATTCAGAGCTTTGATCTCACTCACCTAAACAC	900
QY	901	GAAGCTGCTTTTTCATCTTTTGGAAACCTTTGTTATTTGTTCTCTTAAGTACCTTGCTT	960
DB	901	GAAGCTGCTTTTTCATCTTTTGGAAACCTTTGTTATTTGTTCTCTTAAGTACCTTGCTT	960
QY	961	GGTGTGCAACCGGCTCTGATAGTGCCTATGTTATCAAGAACTATACCTTTGGAAGGCAC	1020
DB	961	GGTGTGCAACCGGCTCTGATAGTGCCTATGTTATCAAGAACTATACCTTTGGAAGGCAC	1020
QY	1021	TCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGGCGTATCTTTCTTATATGCTTGT	1080
DB	1021	TCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGGCGTATCTTTCTTATATGCTTGT	1080
QY	1081	GAGCTTTTTCGACTTCAGCGGTATCTCTCACTGTTGTTTCTGTTGTTATGTTGATGTCCT	1140
DB	1081	GAGCTTTTTCGACTTCAGCGGTATCTCTCACTGTTGTTTCTGTTGTTATGTTGATGTCCT	1140
QY	1141	TACACATGGCACAATGTAACGGAGAGCTCAAGAAATAACAACAAAGCATACCTTTGCAACT	1200
DB	1141	TACACATGGCACAATGTAACGGAGAGCTCAAGAAATAACAACAAAGCATACCTTTGCAACT	1200
QY	1201	TTGTCAATTTCTGCGGAGACATTTATTTTCTTGTATGTTGGATGATGCTTGGACATTT	1260
DB	1201	TTGTCAATTTCTGCGGAGACATTTATTTTCTTGTATGTTGGATGATGCTTGGACATTT	1260
QY	1261	GACAACTGGAGATCCGTGAGTGACACACGGGAAACATCGATCGAGTGAGCTCAATCTTA	1320
DB	1261	GACAACTGGAGATCCGTGAGTGACACACGGGAAACATCGATCGAGTGAGCTCAATCTTA	1320
QY	1321	ATGGGTCTGGTTCATGTTGGAAGAGCAGCTTCTGCTTTTCCGTTATCGTTTCTATCTAAC	1380
DB	1321	ATGGGTCTGGTTCATGTTGGAAGAGCAGCTTCTGCTTTTCCGTTATCGTTTCTATCTAAC	1380
QY	1381	TTAGCCAAAGAAATCAAAGCGAGAAATCAAATTTTAAATGACAGGTTGTTGTTGGTGG	1440
DB	1381	TTAGCCAAAGAAATCAAAGCGAGAAATCAAATTTTAAATGACAGGTTGTTGTTGGTGG	1440
QY	1441	TCTGTCTCATGAGAGGTTGTTGATGCTTATGCTTCTGATGATCAACAAAGTTTCAAGGGCC	1500
DB	1441	TCTGTCTCATGAGAGGTTGTTGATGCTTATGCTTCTGATGATCAACAAAGTTTCAAGGGCC	1500
QY	1501	GGGCAACAGATGTACGGGGAATGCAATCATGATCAGAGTACGATACCTGCTGCTT	1560
DB	1501	GGGCAACAGATGTACGGGGAATGCAATCATGATCAGAGTACGATACCTGCTGCTT	1560
QY	1561	TTTAGCAGAGTGGTGTGTTGTTGATGCTGACCAACCACTCATAAGCTACCTATTACCGCAC	1620
DB	1561	TTTAGCAGAGTGGTGTGTTGTTGATGCTGACCAACCACTCATAAGCTACCTATTACCGCAC	1620
QY	1621	CAGAAACCCCAACGAGCATGTTATCTGATGATCAACACCCCAAAATCCATATATATAT	1680
DB	1621	CAGAAACCCCAACGAGCATGTTATCTGATGATCAACACCCCAAAATCCATATATATAT	1680
QY	1681	TTTGTGGACCAAGACTCTGTTCAATTCAGGCTTCCAGGGAACCAATGCTCGGCTGAC	1740
DB	1681	TTTGTGGACCAAGACTCTGTTCAATTCAGGCTTCCAGGGAACCAATGCTCGGCTGAC	1740
QY	1741	AGTATACGTGGTCTTTGACACGGCCCTCCTCGAACCGTGCATTTACTTGGAGACAAATTT	1800
DB	1741	AGTATACGTGGTCTTTGACACGGCCCTCCTCGAACCGTGCATTTACTTGGAGACAAATTT	1800
QY	1801	GATGACTCTTCACTGCGACCGGCTCTTTGAGAGGTCGTGGCTTTGTTACCTTTGTTCCAGT	1860
DB	1801	GATGACTCTTCACTGCGACCGGCTCTTTGAGAGGTCGTGGCTTTGTTACCTTTGTTCCAGT	1860



Db 1321 TACCTATTACCGCACCAAGACGCCACACAGCATGTTATCTGATGACAAACCCCAAAA 1380  
Qy 1666 TCCATACATATCCCTTTGTTGGACCAAGACTCGTTCAATTGAGCTTTCAGGGAACCAACAAT 1725  
Db 1381 TCCATACATATCCCTTTGTTGGACCAAGACTCGTTCAATTGAGCTTTCAGGGAACCAACAAT 1440  
Qy 1726 GTGCTCGGCTGACAGTATACGTGGCTTTGACACGGCCCACTCGAACCGTGCATTAC 1785  
Db 1441 GTGCTCGGCTGACAGTATACGTGGCTTTGACACGGCCCACTCGAACCGTGCATTAC 1500  
Qy 1786 TACTGGAGACAAATTGATGACTCCTTCATCGACCGCTCTTTGGAGGTCTGTCCTTTGTA 1845  
Db 1501 TACTGGAGACAAATTGATGACTCCTTCATCGACCGCTCTTTGGAGGTCTGTCCTTTGTA 1560  
Qy 1846 CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCCCTCTGATCTTAGTAAGGCTTGA 1902  
Db 1561 CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCCCTCTGATCTTAGTAAGGCTTGA 1617

## RESULT 4

US-09-938-842A-1239  
; Sequence 1239, Application US/09938842A  
; Publication No. US20040009476A9  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE REFERENCE: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCRIPT300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 1239  
; LENGTH: 1617  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-1239

Query Match 74.2%; Score 1617; DB 11; Length 1617;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 286 ATGTTGATTTCTCTAGTGTGAAACGCTTGGTTATCGACATCTGATCAAGCTTCTGTG 345  
Db 1 ATGTTGATTTCTCTAGTGTGAAACGCTTGGTTATCGACATCTGATCAAGCTTCTGTG 60  
Qy 346 GTTGGCTTGAATCTCTTTGTTGACATCTTTGTTGCTTGTATGTTCTTGGTCACTTTTG 405  
Db 61 GTTGGCTTGAATCTCTTTGTTGACATCTTTGTTGCTTGTATGTTCTTGGTCACTTTTG 120  
Qy 406 GAAGAGAAATAGATGGAAGCAAGCAATCCATCAGCGCTTGTGATTGGGCTAGGCACTGGT 465  
Db 121 GAAGAGAAATAGATGGAAGCAAGCAATCCATCAGCGCTTGTGATTGGGCTAGGCACTGGT 180  
Qy 466 GTTACCAATTTGTTGATTAGTAAGGAAAAGCTCGCATCTTCTGTTAGTAGAAGAT 525  
Db 181 GTTACCAATTTGTTGATTAGTAAGGAAAAGCTCGCATCTTCTGTTAGTAGAAGAT 240  
Qy 526 CTTTCTTCATATATCTTTTGGCCACCACTTATATTCATGACGAGGTTTCAAGTAAAGAG 585  
Db 241 CTTTCTTCATATATCTTTTGGCCACCACTTATATTCATGACGAGGTTTCAAGTAAAGAG 300  
Qy 586 AAGCAGTTTTTCCGCAATTTCTGAGCTATATATGCTTTTTTGGTGTCTGTTGGGACTATTAT 645

Db 301 AAGCAGTTTTTCCGCAATTTCTGAGCTATATATGCTTTTTTGGTGTCTGTTGGGACTATTATT 360  
Qy 646 TCTTGACAAATCATATCTCTAGGTGTAAACACAGTTCTTTTAAAGATTGGACATTTGGAACC 705  
Db 361 TCTTGACAAATCATATCTCTAGGTGTAAACACAGTTCTTTTAAAGATTGGACATTTGGAACC 420  
Qy 706 TTTGACTTGGGTGATTAATCTTCTATTTGGTGCCATTAATTTGCTGCAACAGATTCAATGATGT 765  
Db 421 TTTGACTTGGGTGATTAATCTTCTATTTGGTGCCATTAATTTGCTGCAACAGATTCAATGATGT 480  
Qy 766 ACACATGCAAGTTCTGAATCAAGACGAGACACCTTTTGCCTTTTACAGTCTTGTATTCGAGAG 825  
Db 481 ACACATGCAAGTTCTGAATCAAGACGAGACACCTTTTGCCTTTTACAGTCTTGTATTCGAGAG 540  
Qy 826 GGTGTTGTGAATGATGACCAAGCTCAGTTGTGTCTTTCAACGCAATTCAGAGCTTTGATCTC 885  
Db 541 GGTGTTGTGAATGATGACCAAGCTCAGTTGTGTCTTTCAACGCAATTCAGAGCTTTGATCTC 600  
Qy 886 ACTCACCTAAACCAAGAGCTGCTTTTTCATCTTTCTTGGAAACTCTTCTGTAATTTGTTTCTC 945  
Db 601 ACTCACCTAAACCAAGAGCTGCTTTTTCATCTTTCTTGGAAACTCTTCTGTAATTTGTTTCTC 660  
Qy 946 CTAAGTACCTTGTGCTGCTGCAACCGGTCTGATAGTGCATGTTATCAAGAAGCTA 1005  
Db 661 CTAAGTACCTTGTGCTGCTGCAACCGGTCTGATAGTGCATGTTATCAAGAAGCTA 720  
Qy 1006 TACTTTTGAAGGCACTCAACTGACGAGAGTTGCTTATGATGCTTATGCGGTATCTT 1065  
Db 721 TACTTTTGAAGGCACTCAACTGACGAGAGTTGCTTATGATGCTTATGCGGTATCTT 780  
Qy 1066 TCTTATATGCTTGTGAGCTTTTTCGACTTGTGAGCGGTATCTTCACTGTGTGTTTCTGTGT 1125  
Db 781 TCTTATATGCTTGTGAGCTTTTTCGACTTGTGAGCGGTATCTTCACTGTGTGTTTCTGTGT 840  
Qy 1126 ATTGTGATGTCCCATTAACATGCGCAAAATGTAAACGAGAGCTCAAGAAATAACAACAAG 1185  
Db 841 ATTGTGATGTCCCATTAACATGCGCAAAATGTAAACGAGAGCTCAAGAAATAACAACAAG 900  
Qy 1186 CATACCTTTGCAACTTTGCTCACTTTCTGCGGAGACATTTATTTCTGATGCTGGAATG 1245  
Db 901 CATACCTTTGCAACTTTGCTCACTTTCTGCGGAGACATTTATTTCTGATGTTGGAATG 960  
Qy 1246 GATGCTTTGGACATTTGCAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1305  
Db 961 GATGCTTTGGACATTTGCAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1020  
Qy 1306 GTGAGCTCAATCTCTAATGGTCTGCTCATGTTGGAAGAGAGCGTTTCTGTTCCGTTA 1365  
Db 1021 GTGAGCTCAATCTCTAATGGTCTGCTCATGTTGGAAGAGAGCGTTTCTGTTCCGTTA 1080  
Qy 1366 TCGTTTCTATCTAATGGTCTGCTCATGTTGGAAGAGAGCGTTTCTGTTCCGTTA 1425  
Db 1081 TCGTTTCTATCTAATGGTCTGCTCATGTTGGAAGAGAGCGTTTCTGTTCCGTTA 1140  
Qy 1426 GTTGTGATTTGGTGTGCTGCTCATGAGAGGTGCTGATCTATGGCTCTTTCGATACAAAC 1485  
Db 1141 GTTGTGATTTGGTGTGCTGCTCATGAGAGGTGCTGATCTATGGCTCTTTCGATACAAAC 1200  
Qy 1486 AAGTTTACAAGGCGCGGCAACAGATGTAACGCGGAATGCAATCATGATCAGAGTACG 1545  
Db 1201 AAGTTTACAAGGCGCGGCAACAGATGTAACGCGGAATGCAATCATGATCAGAGTACG 1260  
Qy 1546 ATAACTGTCTCTTTTGTAGCACAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1605  
Db 1261 ATAACTGTCTCTTTTGTAGCACAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1320  
Qy 1606 TACCTATTACCGCACAGAACCCACACGAGCATGTTATCTGATGACAAACCCCAAAA 1665  
Db 1321 TACCTATTACCGCACAGAACCCACACGAGCATGTTATCTGATGACAAACCCCAAAA 1380  
Qy 1666 TCCATACATATCCCTTTTGTGGAACAGACTCGTTTCAATTTGAGCCTTTCAGGGAACCCCAAT 1725  
Db 1381 TCCATACATATCCCTTTTGTGGAACAGACTCGTTTCAATTTGAGCCTTTCAGGGAACCCCAAT 1440

Qy	1726	GTGCTCGGCTGACAGATATACGTGGCTCTTTGACACGGCCCACTCGAACCGTGCATTAC	1785
Db	1441	GTGCTCGGCTGACAGATATACGTGGCTCTTTGACACGGCCCACTCGAACCGTGCATTAC	1500
Qy	1786	TACTGGAGACAATTGTATGACTCCTTCATGGGACCCGTCCTTTGGAGTCTGTGGCTTTGTA	1845
Db	1501	TACTGGAGACAATTGTATGACTCCTTCATGGGACCCGTCCTTTGGAGTCTGTGGCTTTGTA	1560
Qy	1846	CCCTTTGTTTCAGGTTCTCCAACTGAGAGAAACCTCTCGATCTTATAGGCTTGA	1902
Db	1561	CCCTTTGTTTCAGGTTCTCCAACTGAGAGAAACCTCTCGATCTTATAGGCTTGA	1617

## RESULT 5

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US-10-155-535-1
US-10-155-535-1
; Sequence 1, Application US/10155535
; Publication No. US20030046729A1
; GENERAL INFORMATION:
; APPLICANT: Blumwald, Eduardo
; APPLICANT: Apse, Marie
; TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY
; EXPRESSION OF VACUOLAR CATION-PROTON ANTIPORTERS
; FILE REFERENCE: 529152000720
; CURRENT APPLICATION NUMBER: US/10/155,535
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 09/271,584
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,474
; PRIOR FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: 60/116,111
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2136
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-155-535-1

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Query Match	52.8%;	Score 1149.4;	DB 14;	Length 2136;
Best Local Similarity	81.5%;	Pred. No. 6.3e-274;		
Matches 1362;	Conservative 0;	Mismatches 291;	Indels 18;	Gaps 2;
Qy	272	AGAAAGAGATAACAATGTTGGATTCTCTAGTGTGGAAACTGCCTTCGTATTCGACATCTG	331	
Db	353	AAAGAAAGATGACAAATGTTGCCTCTTTAACTCTAAATGCTATCGGTCTCAACTTCG	412	
Qy	332	ATCAGCTTCTGTGGTTCGTTGAATCTCTTTGTTGGACATCTCTTTGTCGTGTGATTGTTTC	391	
Db	413	ATCAGCGATCTGTCTTTTCACTTAATCTCTTTGTTGCCTTCTATGTGCTTGTATCGTCA	472	
Qy	392	TTGTGTCATCTTTTGGAAGAGAATAGATGGATGAACGAATCCATCACCGCTTGTGTGATTG	451	
Db	473	TTGGCCATCTTTTGGAGAGAAATCGATGGATAACGAATCCATCACTGCTTTTATGTGATTG	532	
Qy	452	GGCTAGGCACCTGGTGTATACCATTTTGTGTGATTAGTAAAGGAAAAAGCTCGCATCTCTTCG	511	
Db	533	GGCTTGGCACCTGGTGTCTGTCATATGTTGTGATTAGTAGAGGGAAAACTCACATCTCTTTG	592	
Qy	512	TCATTAGTGGAGATCTTTTCTCATATATCTTTTGGCCACCATTATATTTCAATGCAGGCT	571	
Db	593	TCATTAGTGAAGATCTCTCTTTATATATCTTTTGGCCACCATAAATTCAAATGCAGGGT	652	
Qy	572	TTCAAGTAAAAAAGAAGCAGTTTTTCCGCAATTTTCGTGACTATTATATCTTTTTTGGTGCTG	631	
Db	653	TTCAAGTAAAAAAGAAGCAGTTTTTCCGAAATTTTGTAACTATTATGCTTTTTTGGCGCCA	712	
Qy	632	TTGGGACTATATTTCTTTGGACATCATATCTCTAGGTGTAAACAGTTCCTTTAAGAACT	691	
Db	713	TTGGGACCGTAGTTTCTTTGCAACCAATAATCTCTAGGTGTCAATTCAGTTCCTTTAAGAAAT	772	
Qy	692	TGGACATTGGAACCTTTTGACTTTGGGTGATTATCTTGTCTATTGTGTGTCATATTTTGTGTCGAA	751	

[illegible]

Db 1853 TCCTCATGCGCCCCACACGAGCTGTCCACTATTAATCTGGAGACAGATTTGATGATGCGCTTCA 1912  
Qy 1814 TGGACCCGCTTTTGGAGTCTGCTGCTTTGTATACCTTTTGTTCAGGTTCTTCCAACTGAGA 1873  
Db 1913 TGGCTCCTGTGTTGTTGGTGTGGGATTCGTTCCCTTTGTCCCTGCTCCGACTGAGA 1972  
Qy 1874 GAACCCCTCTGATCTTAGTAGGCTTGGAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTT 1924  
Db 1973 GAAGCAGCCATGATCTTAGTAACCTTGAAGACCTTGAAGGAGAAATATATAGAAACTT 2023

## RESULT 6

US-11-067-456-1

; Sequence 1, Application US/11067456

; Publication No. US20050144666A1

; GENERAL INFORMATION:

; APPLICANT: Blumwald, Eduardo

; APPLICANT: Apse, Marib

; TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY

; FILE REFERENCE: OVEREXPRESSION OF VACUOLAR NA+/H+ TRANSPORTERS

; CURRENT APPLICATION NUMBER: US/11/067,456

; CURRENT FILING DATE: 2005-02-24

; PRIOR APPLICATION NUMBER: 10/155,535

; PRIOR FILING DATE: 2002-05-24

; PRIOR APPLICATION NUMBER: 09/271,584

; PRIOR FILING DATE: 1999-03-18

; PRIOR APPLICATION NUMBER: 60/078,474

; PRIOR FILING DATE: 1998-03-18

; PRIOR APPLICATION NUMBER: 60/116,111

; PRIOR FILING DATE: 1999-01-15

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 2136

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-11-067-456-1

Query Match 52.8%; Score 119.4; DB 24; Length 2136;  
Best Local Similarity 81.5%; Pred. No. 83; 274; Indels 18; Gaps 2;  
Matches 1362; Conservative 0; Mismatches 291;

Qy 272 AGAAGAGATAACAATGTTGGATCTCTAGTGTGGAACCTGCTTATCGAATCTG 331  
Db 353 AAAGAAAGATGACAATGTTGCGCTCTTAACTCTAAATGCTATCGGTGCACTCTG 412  
Qy 332 ATCAGCTTCTGTGTTGGTGTGAATCTCTTTGTTGCACTTCTTTGTTGCTTGTATGTTTC 391  
Db 413 ATCAGCATCTGTGTTTCACTTAATCTCTTTGTTGCGCTTCTATGTGCTTGTATCGTCA 472  
Qy 392 TTGGTCATCTTTTGAAGAGATAGATGATGATGATGATGATGATGATGATGATGATGATG 451  
Db 473 TTGGTCATCTTTTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 532  
Qy 452 GGTAGGCACTGTTGTTACCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 511  
Db 533 GGTAGGCACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 592  
Qy 512 TCTTAGTGAAGATCTTTTCTCATATATCTTTTGGCCACCCATATATTTCAATGAGGTT 571  
Db 593 TCTTAGTGAAGATCTTTTCTCATATATCTTTTGGCCACCCATATATTTCAATGAGGTT 652  
Qy 572 TTCAAGTAAAGAGAGAGAGTTTTCGCAATTTCTGACTATATGTTTGTGTTGTTGTTGTTG 631  
Db 653 TTCAAGTAAAGAGAGAGAGTTTTCGCAATTTCTGACTATATGTTTGTGTTGTTGTTGTTG 712  
Qy 632 TTGGAGTATTTATTTCTTGCACATCATATCTCTAGGTGTAAACAGATTTCTTTAAGAGT 691  
Db 713 TTGGAGTATTTATTTCTTGCACATCATATCTCTAGGTGTAAACAGATTTCTTTAAGAGT 772  
Qy 692 TGGACATTTGGAACCTTTGATTTGGTGTGATTAATCTTGTCTATTGGTGCCATATTTGCTGCA 751

Db 773 TAGACATTTGGGACCTTTGACTTTGGCGGATTTTCTTGCAATCGCGCCCATATTTTGTGCAA 832  
Qy 752 CAGATTCAGTATGTACACTGCAAGTTCTGAATCAAGAGAGAGACACTTTGTTCTTTACAGTC 811  
Db 833 CCGACTCTGTATGCACACTACAGTTCTCAATCAAGATGAGACACTTTGTTCTTTACAGTC 892  
Qy 812 TTGTATTCGGAGAGGTTGTTGTAATGATGCAACGTCAAGTTGTGTGTTCTTCAACGCAATTC 871  
Db 893 TTGTATTTGGAGAGGCGTTGTAATGATGCCACATCTGTTGTGCTCTTCAATGCTATTC 952  
Qy 872 AGAGCTTTGATCTCACTCACTTAACCAAGAGAGCTTCTTTTCATCTTCTTGAACACTTCT 931  
Db 953 AGAGTTTGTGACCTCAACCACTTAAACATGAAGCAGCTTTTCAATTTCTTGGGAACTTTT 1012  
Qy 932 TGTATTTGTTTCTTCTTAAGTACCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 991  
Db 1013 TTTATCTGTTTCTTGTGACACCGGACTTGTGTGCGCACTGTTCTGATGATGATGATGATG 1072  
Qy 992 TTATCAAGAGCTATATCTTTTGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATGC 1051  
Db 1073 TCATCAAGAACTGTATTTTGAAGGCACTCGACTGATCGAGAACTTGCCTCATGATGC 1132  
Qy 1052 TTATGGCGTATCTTCTTATATGCTTGTGAGCTTTTCGACTTGTAGCGGTATCCTCAGTC 1111  
Db 1133 TTATGGCTTATCTTTTATATATGCTTGTGAGCTTATCGCTTGTAGTGTATCTCTAAGTC 1192  
Qy 1112 TGTTTTCTGTGTTATGTTGATGTCCTCATTAACATGACCAATGTAACGAGAGCTCAA 1171  
Db 1193 TATTTTCTGTGGATGTTGATGTTCCCAATTAACCTTGGCAATGTCACCGAGAGCTCAA 1252  
Qy 1172 GAATAACAACAAAGCATACCTTTGCACTTTGTCTATTTCTTGTGCGGAGACATTTATTTCT 1231  
Db 1253 GAATTTACTACCAAGCATGCCCTTGTCTTCTTGTGCTTCTGCTGAGACTTTTATTTTCC 1312  
Qy 1232 TGTATGTTGGAATGATGATGCTTGGACATGACAGTGGAGATTCCTGATGACACACCGG 1291  
Db 1313 TCTAGTTTGAATGGAATGCAATTTGGACATAGAGAAATGGAGATTCGTGATGACACCGG 1372  
Qy 1292 GAAACATGATCGAGTGTGCTCAATCTTAATGGGTCTGCTCATGTTGTTGGAAGAGAGCT 1351  
Db 1373 GGACATGATTTGAGTGTGCTCAATCTTAATGGGTCTGCTCATGTTGTTGGAAGAGAGCT 1432  
Qy 1352 TCCTTTTCTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1411  
Db 1433 TTGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1492  
Qy 1412 ACTTTAATGATGAGTGTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1471  
Db 1493 GCATCAAGCAGCAAGTTGTGATCTGTTGGGCTGTTCTAATGAGAGGTTGCTGTATCTATGG 1552  
Qy 1472 CTCTTGCAACAACAAGTTTACAGGGCCGGGCAACAGATGTACCGGGGATGCAATCA 1531  
Db 1553 CTCTTGCTCAACAATGATTTACAGATCAGGGGCAACAGATTTGCGGGGATGCAATCA 1612  
Qy 1532 TGATCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1591  
Db 1613 TGATCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1672  
Qy 1592 AACCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1642  
Db 1673 AACCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1732  
Qy 1643 TATCTGATGACACACCCCAAAATCCATATATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1693  
Db 1733 TATCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1792  
Qy 1694 ACTGTTTCTTGTGAGCTTTCAGGGAACCAATGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 1753  
Db 1793 ATTCAATTTGATTTACCTGGGAGCCACAGGAGCTTGTGCAACCAACAGCTTTCGAGTT 1852  
Qy 1754 TCTTGACACGCCCACTGCAACCGGTGCAATTAATCTTGTGAGACAAATTTGATGATCTCTTCA 1813  
Db 1853 TCCTCATGCGGCCCAACAGGAGCTGTCCACTATTACTTGTGAGACAGATTTGATGATGATGAT 1912





Qy	1814	TCGACCCGCTCTTTGGAGGTCGTGCTTTGTATACCTTTGTTCACAGGTTCTCAACTGAGA	1873
Db	1913	TGCGTCTCTGTGTTTGGTGGTCGCGGATTCGTTCCCTTTGTTCCTCGACTGAGA	1972
Qy	1874	GAAAACCCCTCCCTGATCTTAGTAGGCTTCAGGAGTAACTGGAAGAAAGCTT	1924
Db	1973	GAAGCAGCCATGATCTTAGTAACTTCGAGGGAAGATATATAGAACTT	2023
<p>RESULT 8</p> <p>US-10-425-114-20609</p> <p>: Sequence 20609, Application US/10425114</p> <p>: Publication No. US20040034888A1</p> <p>: GENERAL INFORMATION:</p> <p>: APPLICANT: Liu, Jingdong</p> <p>: APPLICANT: Zhou, Yihua</p> <p>: APPLICANT: Kovalic, David K.</p> <p>: APPLICANT: Green, Steven E</p> <p>: APPLICANT: Tabaska, Jack E</p> <p>: APPLICANT: Cao, Yongwei</p> <p>: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With</p> <p>: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement</p> <p>: FILE REFERENCE: 38-21(5313)B</p> <p>: CURRENT APPLICATION NUMBER: US/10/425,114</p> <p>: CURRENT FILING DATE: 2003-04-28</p> <p>: SEQ ID NO 20609</p> <p>: LENGTH: 1915</p> <p>: TYPE: DNA</p> <p>: ORGANISM: Glycine max</p> <p>: FEATURE:</p> <p>: OTHER INFORMATION: Clone ID: LIB3242-431-A12_FLI</p> <p>US-10-425-114-20609</p>			
<p>Query Match 38.4%; Score 837.4; DB 18; Length 1915;</p> <p>Best Local Similarity 71.2%; Pred. No. 1.3e-196;</p> <p>Matches 1143; Conservative 0; Mismatches 441; Indels 21; Gaps 2;</p>			
Qy	294	TTCTCTAGTGTGAAATGCGCTTCGTTATCGACATCTGATCACGCTTCTGTGGTTGCGTT	353
Db	2	TTCTGTGTTTCAAAATTTGCAACGTTATCCACCTCAGACCATGCTCCGTGGTCTCCAT	61
Qy	354	GAATCTCTTTGTGTCATCTTTTGTGCTGTATGTTCTTGGTCACTCTTTTGGAAAGAA	413
Db	62	GAACCTTATTTGTGGCAGCTTCTTTGTGGTTGTATTTGCTCTGGCCATCTTCTTGAGAGAA	121
Qy	414	TAGATGATGAACGAATCCATCCATCCGCTTTGTTGATTTGGCTAGGCACTGGTGTACCAT	473
Db	122	TCGATGATGAACAGCAGTCTATCATCGCCCTTTGATTTGGTGTGTCACCTGGCGTAGTCAT	181
Qy	474	TTTGTGTAATTAGTAAAGGAAAGAGCTCGCATCTTCTCGTCTTTAGTGAAGATCTTTTCTT	533
Db	182	TTTGCTGTTTAGTGGTGCAGAAAGCTCACATATCTTGTTTTCAGTGAAGATCTTTTCTT	241
Qy	534	CATATATCTTTTGGCCACCATTTATATTCAGTCAGGGTTTCAAGTAAAAAAGAACGATT	593
Db	242	TATATATCTTACACCATTAATATTCATGCGGGTTTTCAGGTGAAAAAAGAACGATT	301
Qy	594	TTTCCGCATTTCTGTGACTATATGCTTTTGGTGCTGTTGGGACTATATTTCTTGTGAC	653
Db	302	TTTTTGTAACTTTCATGACCATCATGTGTTGGTGCTATTGGTACATTAATATCATGTAC	361
Qy	654	AATCATATCTCTAGTGTAAACACAGTCTCTTAAAGAAAGTTGGACATTTGGAACCTTTGACTT	713
Db	362	CATCATAACTTTGGGTGCCACAAATTTTAAAGAGTTTGGATGTTGGTCTCTCGAATT	421
Qy	714	GGGTGATTATCTTGCTATTGGTGCCATATTTGCTGCAACAGATTTCAGTATGTACACTGCA	773
Db	422	AGGGGATTTCTAGCAATTTGGTGCAATATTTGCTGCAACGGATTCTGTTGGCACATTGCA	481
Qy	774	GGTTCTGAATCAAGACAGACACCTTTGCTTTTACAGTCTTGTATTTCCGAGAGGGGTGTGT	833
Db	482	GGTGCTAAATCAGGATGAGACACCTTTGCTGTACAGTCTTGTATTTGGGAGGGGTGTGT	541



RESULT 9  
US-10-424-599-58707  
; Sequence 58707, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 58707  
; LENGTH: 1968  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MFT3847\_24023C.1  
US-10-424-599-58707  
  
Query Match 37.7%; Score 821.8; DB 18; Length 1968;  
Best Local Similarity 70.6%; Pred. No. 9.8e-193;  
Matches 1134; Conservative 0; Mismatches 452; Indels 21; Gaps 2;  
  
QY 292 GATCTCTAGTGTGGAAGCTGCTTCGTTATTCGACATCTGATCAGCTTCTGTGTGCG 351  
DB 16 GGTTCGTGTTTCAAAATGCAACGTTATCCACCTCAGACCATGCTCGTGTCTCC 75  
  
QY 352 TTGAATCTCTTGTGTCATCTTCTGTGCTGTATGTTCTTGTGTCATCTTTTGAAGAG 411  
DB 76 ATGAACTATTATGTCGCACTTCTTGTGCTGTATGTTCTTGTGCACTTCTTTGAGGAG 135  
  
QY 412 AATGATGATGAAGCAATCCATCACCCTGTTGTTGATTTGGCTAGGCACTGTTGTTACC 471  
DB 136 AATCGGTGATGAACAGTCTATCACTGCTCTTTGATTTGGTGTTCGACCTGGCATTGTC 195  
  
QY 472 ATTTTGTGTTAGTAAAGGAAAAAGCTCGCATCTTCTCGTCTTTTGTGTAAGATCTTTTC 531  
DB 196 ATTTGCTGTTTGTGTTGGGCAAGCTCGCATATCTTGTGTTTTCAGTGAAGATCTTTTC 255  
  
QY 532 TTCAATATCTTTTCCGACCCCATATATATCAATGACAGGTTTCAAGTAAAAAAGAACGAG 591  
DB 256 TTATATACCTTCTACCACTATAATATTTAATGCCGGTTCAGGTGAAAAAAGAACGAG 315  
  
QY 592 TTTTATCCGCAATTCGTCATATATGCTTTTGTGCTGTTGGGACATATTATTTCTTTC 651  
DB 316 TTTTGTGTTAACTTCATGACCATCATGTTGTTGTTGCTATTTGGTACATTAATCATGT 375  
  
QY 652 ACAATCATATCTCTAGGTGTAACACAGCTTCTTTAAGAAAGTTGGACATTTGGAACCTTTGAC 711  
DB 376 ACCATCATAACTTTGGGTGCCACAAATTTTAAAGAGTTGGATGTTGGTCTCTGGAA 435  
  
QY 712 TTGGGTGATATCTGCTATTGGTGCCATATTTGCTGCAACAGATTAGTATGATACATG 771  
DB 436 TTAGGGGATTTCTAGCAATTTGGTGAATATTTGCTGCAACGGATTCGTTTGACATTTG 495  
  
QY 772 CAGGTCTGAATCAAGACGAGACCTTTGCTTTACAGTCTTGTATTCGGAGAGGGTGT 831  
DB 496 CAGGTCTGAATCAGATGAGACCTTTGCTGTAAGTCTTGTATTTGGGAGGGTGT 555  
  
QY 832 GTGAATGATGCAACGTCAGTTGTGCTTCTCAACGCGATTTCAGAGCTTTGATCTCACTCAC 891  
DB 556 GTGAATGATGCTACATCAGTGTGCTTTTCAATGCAATCCAAAGCTTTGACCTCAACCAA 615  
  
QY 892 CTAACACGAGAGCTGCTTTTCTCTTGTGAAACTTCTGTTATTTGTTCTCTCTAGT 951  
DB 616 ATTGACTCTCAATTTGCTGTACACTTTTGGGAAATTTCTTGTATCTATTTATTTGCAAGC 675  
  
QY 952 ACCTTTGTGTTGCTGCAACCGTCTGATAAGTGGTATGTTATCAAGAAGCTATACTTT 1011

DB 676 ACAATGCTTGGAGTTTTCACAGGTCTACTTACTTACATTTAAAGAGCTGACATT 735  
QY 1012 GGAAGGCACTCAACTGACCCGAGAGGTTGCCCTTATGATGCTTATGGGCTATCTTTCTTAT 1071  
DB 736 GGCAGGCACTCTACAGATCGTGGAGTTGCTCTTATGATGTTAATGGCATACCTGCTCTAC 795  
QY 1072 ATGCTTGTGAGCTTTTTCGACTTGGAGCGGTATCTCTCACTGTTGTTTCTGTTGGTATTTG 1131  
DB 796 ATGCTTGTGAAATATGTTATCTGAGTGGCAATCTCTCACTGTTATCTTTTGGTATTTGTT 855  
QY 1132 ATGTCCTCATACATGGCAATGTAACGAGAGCTCAAGAAATAACAACAAGACATACC 1191  
DB 856 ATGCTCTATATACCTGGCATACGTCAGCCGAGAGTTCAAGAACTCACTACCAAGCATCT 915  
QY 1192 TTTGCAACTTTTGTCAATTTCTTGGGAGACATTTATTTTCTTGTATGTTGGAATGGATGCC 1251  
DB 916 TTTGCAACCTTGTCTTTTGTGCTGAGATCTTTATCTTCTCTTATGTTGTTGGTATGGATGCC 975  
QY 1252 TTGGACATTTGACAGTGGAGATCCGTGAGTGACACCGGGAACATCGATCGCAGTGGAGC 1311  
DB 976 TTGGACATTTGAAATGAAATTTGTGAGTGATAGCCCTGGAACTCTGTAGCAACTAGT 1035  
QY 1312 TCAATCTTAATGGGTCTGGTCAATGTTTGGAGAGCAGCGTTTCGTCTTTTCCGTTATCGTTT 1371  
DB 1036 TCAGCTTATTTCTGCTAAATCTTCTTGTGGAAGACAGCTTTTGTTCCTTATCCTTC 1095  
QY 1372 CTATCTAACTTAGCCAAAGAAATCAAAAGCGAGAAATCAACTTTTAAATGATGCAAGTTGTG 1431  
DB 1096 ATATCCAACTTTGGCTAAAAAATCAACCAATGAGAAAAATCAGCTTCAGACAGCAAGTGATC 1155  
QY 1432 ATTTGTTGTTGCTGCTCATGAGAGGTCGTATCTATGCTCTTGTGATACCAAGTTT 1491  
DB 1156 ATTTGTTGTTGCTGCTCATGAGAGGTCGTATCTTCAATCGCACTTGATATATCAAGTTT 1215  
QY 1492 ACAAGGCGCGGGCACACAGATGTACGGGGAAATGCAATCATGATCAGAGTACGATTAAT 1551  
DB 1216 ACCATGTCGGGGCACACTTCTCACTCGGAAGCAATGCAATCATGATCACAAGCACCATCACT 1275  
QY 1552 GTCTGTCTTTTATGACAGTGGTGTGTTGGTATGCTGACCAAAACCACTCATTAAGCTACCTA 1611  
DB 1276 GTTGTGCTTTTTCAGCACAGTGGTGTGTTGGTCTGTTGACTAAGCCACTCATAAGGCTTTTA 1335  
QY 1612 TT-----ACCGCACCAAGACCGCACAGAGCATGTTATCTGTATGACAAACACC 1659  
DB 1336 CTGCCCCATCTCCACATCATAAAGAAATCAAGCATCAGATAATCAAGATCCATCTACT 1395  
QY 1660 CCAAAATCCATACATATCCCTTTTGTGGACCAAGACTCGTTTCATTGAGCCTTCAGGGAA - 1718  
DB 1396 CCAAGTCCAAATCAGTCACCTATCCCACTTCTTGGAGTGCCTCAAGAAATCTGAAGTTGAT 1455  
QY 1719 -----CCAAATGTGCTCGGCTGACAGTATAGTGTGCTTTCATTGAGCCTTCAGGGAA - 1770  
DB 1456 ATCGATGCCCATGATATTCATCGTCAAGCAGTATTCGTGCTTGTGCTTGTGACAGCGCCACT 1515  
QY 1771 CGAACCTGTGATTAATACTGAGCAATTTGATGATCTCTTTCATGCGACCGCTCTTTGGA 1830  
DB 1516 CACACTGTTTCATGCTTGTGCGGTAAGTTTGAATGATGATTCATGCTGCTCTGTTTGGT 1575  
QY 1831 GGTGCTGCTTGTGATCCCTTTGTTTCCAGGTTTCTCCAACTGAGAGAA 1877  
DB 1576 GGCAGGGGTTTGTCTCTGTAGAACCTGGCTCCACCACTGAACGTAA 1622

RESULT 10  
US-10-369-324-38  
; Sequence 38, Application US/10369324  
; Publication No. US20030221213A1  
; GENERAL INFORMATION:  
; APPLICANT: ROMMENS, CAIUS  
; APPLICANT: YE, JINGSONG  
; APPLICANT: MENENDEZ-HUMARA, JAIME  
; APPLICANT: YAN, HUA

APPLICANT: RICHARD, CRAIG  
APPLICANT: BRINKERHOFF, W. LEIGH  
APPLICANT: SWORDS, KATHY M. M.  
TITLE OF INVENTION: PRECISE BREEDING  
FILE REFERENCE: 058951/0162  
CURRENT APPLICATION NUMBER: US/10/369,324  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/357,661  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: 60/377,602  
PRIOR FILING DATE: 2002-05-06  
NUMBER OF SEQ ID NOS: 124  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 38  
LENGTH: 1620  
TYPE: DNA  
ORGANISM: Solanum tuberosum  
US-10-369-324-38

Query Match 36.6%; Score 797.6; DB 17; Length 1620;  
Best Local Similarity 69.3%; Pred. No. 8.8e-187;  
Matches 1101; Conservative 0; Mismatches 484; Indels 3; Gaps 1;

QY 287 TGTGGATTCCTAGTGTGGAACCTGCTTGGTATCGACATCTGATCAGGCTTCGTGG 346  
DB 11 TGTGGCTTCTCTGTTTCCAAACCTGGGCTCTTTGGGTACTTTCAGATCATGCTTCTGTG 70

QY 347 TTGCGTTGAATCTCTTTGTTGCACTTCTTTGCTTGTATGTTCTTTGGTCACTTTTGG 406  
DB 71 TATCCATCAACCTCTTTTGGCACTCTTTTGTCTTGCATCATCATTTGTCATCTCTTGG 130

QY 407 AAGAGAAATAGATGATGAACGATCCATCAACCGCTTGTGATTTGGCTTAGGCATCTGGTG 466  
DB 131 AGGAGAACCGCTGGGTTATGAGTCCATTTACTGCCCTCATATTTGTTGTGTACAGGAG 190

QY 467 TTACCAATTTTGTGATGATGAAGAAAGCTTGGCATCTTCTGCTTTTGTAGTGAAGATC 526  
DB 191 TGGTTATCTTGTGCTGTAAGTGGTGAAGAACTCAACCTCTCTGTTTTCAGTGAAGATC 250

QY 527 TTTTCTTCATATATCTTTTCCACCATATATTAATGCAAGGCTTCAAGTAAAGAAAGA 586  
DB 251 TCTTTTTCATATATGATCTTCTTCCAAATCATATTTAATGAGGCTTTCAGGTAAGAAAGA 310

QY 587 AGCAGTTTTTCCGCAATTTCTGCTATTTATGCTTTTGGTCTGTTGGGCACTATTATTT 646  
DB 311 AGCAATTTTCTGTAATCTTACTATATATGATGTTTCGAGCCATTTGTTACCTGGTCT 370

QY 647 CTTGCAATATATCTCTAGGTGTAACAAGCTTCTTTAAGAAAGTTGGACATTTGAACCT 706  
DB 371 CATGTGCCATATATCATTTAGGTGCAATTTCAAACTTTCAAGAAAGTTGGACATTTGAATTC 430

QY 707 TTGACTTGGGTGATATCTGCTATTTGTTGGTCCATATTTCTGCAACAGATTCAGTATGTA 766  
DB 431 TAGATATGGGATATATCTTGAATTTGGAGCAATATTTGCTGCCACAGATTCGGTCTGCA 490

QY 767 CACTGCAGGTCTCTGAATCAAGAGAGACACCTTTGCTTTACAGTCTTGTATTTCGAGAGG 826  
DB 491 CATTGCAGGTCTCTACATCAGGATGAGACACCTCTTTTACAGTCTTGTATTTCGAGAG 550

QY 827 GTTGTGTGAATGATCAACGCTCAGTTGTGTTGCTTCAACGCGATTCAGAGCTTTGATCTCA 886  
DB 551 GAGTTGTAATGATGCTACATCGGTGCTTCTTCAATGCTATTCAAAACCTTTGACCTTA 610

QY 887 CTCACCTAAACACGAGAGCTCTTTTCATCTTCTTGGAACTCTTGTATTTGTTTCTCC 946  
DB 611 CGAGCGTGAATCCCAATAGCCCTCAGTTTCTTGGCAACTCTTCTATCTGTTCTCTTG 670

QY 947 TAAGTACCTTGTGTTGCTGCAACCGGCTGATAGTGCATGTTATCAAGAAAGCTAT 1006  
DB 671 CTAGCACTTTACTGGAGCAGGAACTGGTCTTCTTAGTGCTTACATTTCAAGAAAGCTGT 730

QY 1007 ACTTTGGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGGGCTATCTTT 1066

DB 731 ATTTGGCAGGCACCTCCACAGATCGTGAAGTTGCCCTTATGATGCTCATGGCTTACTTAT 790  
QY 1067 CTTATATGCTTCTGCTGAGCTTTTCCGACTTTGAGCGGTATCTCTCACTGTGTTTCTGTGTA 1126  
DB 791 CATACATGCTGGTGAATCTTATTTGAGTGGGATCTCACTGTATTTTCTGTGTA 850  
QY 1127 TTGTGATGTCCCATTTACATGCGCAATGTAAACGAGAGCTCAAGAAATAACAACAAGC 1186  
DB 851 TTGTAAATGTCTCATTTACACTTGGCAATGTGACCGAGAGTTCAAGAGTCACTACAAGC 910  
QY 1187 ATACCTTTGCACTTTTGTCTTCTGCGGAGACATTTATTTCTTGTATGTTGGAATCG 1246  
DB 911 AGCTTTTTCGAATTTTGTCTTTTTCAGAGACTTCTCTCTCTATGTCGGCATGG 970  
QY 1247 ATGCTTTGGAATTTGACAAAGTGGAGATCCGTGAGTGACACACCGGAAACATCGATCGCAG 1306  
DB 971 ATGCTTTGGATATCGAAGTGGAAATTTTGTGTTGACAGGCTGGATATCAATTTCCG 1030  
QY 1307 TGAGCTCAATCCTAATGCGTCTGTCATGTTTGAAGAGCAGCGTTCGTCTTTTCCGTAT 1366  
DB 1031 TGAGTTCAATATCTGATGGGATTAATCTTGTGGGAGAGCTGCCCTTTGTTTTCATAT 1090  
QY 1367 CGTTTCTATCTAACTTACCCAGAGAAATCAAGCGAGAAATCACTTTAAACATGCGAG 1426  
DB 1091 CATCTTCTCAACTTAATGAAGAAATCCTCGAGCAAAATAATACCTTTAGGCGAGCAG 1150  
QY 1427 TTGTGATTTGGTGTCTGCTCTCATGAGAGGTGCTGTATCTATGCTCTTGTGATCAACA 1486  
DB 1151 TGATATATGTTGGCAGGTTTGTATGAGGCGGAGTGTCCATGCGACTGGCATATATA 1210  
QY 1487 AGTTTAAAGGCGCGGCGACACAGATGTAACGCGGAATGCAATCATGATCAGAGTACGA 1546  
DB 1211 AGTTCACTCGTGGGGGACACACTCACTCACTGCAGGACAATGCAATAATGATTACCAGCAG 1270  
QY 1547 TAACTGTCTGCTTTTATAGCAGGTGTTGTTGTTGATGCTGACCAAAACCACTCATAGCT 1606  
DB 1271 TAAACATTTGTTCTATTTACGACAAATGTTGCTTAAATGACAAAACCCCTTATAAGTC 1330  
QY 1607 ACCTATTACCGCACCAGAAAGCCACGAGAGCTGTTATCTGATGACAAACCCCAAAAT 1666  
DB 1331 TCTGCTGCCACACAGAGGCAATTTGAGTACAGTGTCTATCAGGTGCAAAATCTCCAAAGT 1390  
QY 1667 CCATACATATCCCTTTTGTGGAC---CAAGACTCGTTTCATTTAGCGCTTCAGGGAACCA 1723  
DB 1391 CTCCTAACAGCCCACTCTCTAGCAGTCGAGAGGACTCTGAAAGTTGATTTAAATGTTCCAG 1450  
QY 1724 ATGCGCTCGGCTGACAGTATACGTGGCTTCTTGAACGGCCCACTGGAACCGTGCATT 1783  
DB 1451 ATCTTCTCTACCCCAACAAAGTTTGAGGATGCTACTTTACCGCACCAAGTCATAAAGTGCATC 1510  
QY 1784 ACTACTGGAGACAATTTGATGACTCCTTTTCATGCGACCGCTCTTTGAGAGTCTGCTGCTTG 1843  
DB 1511 GGTACTGGGCAAGTTTACGATGATTCATGCGGCCCTATGTTTGTGTCGGGATTTG 1570  
QY 1844 TACCTTTTGTTCAGGTTCTCCAACTGA 1871  
DB 1571 CTCCTCTGCCCCCTGTTCTCCACGGA 1598

RESULT 11  
US-10-607-538-38  
Sequence 38, Application US/10607538  
Publication No. US20040107455A1  
GENERAL INFORMATION:  
APPLICANT: ROMMENS, CAIUS  
APPLICANT: YE, JINGSONG  
APPLICANT: HUMARA, JAIME M.  
APPLICANT: YAN, HUA  
APPLICANT: SWORDS, KATHY  
TITLE OF INVENTION: PRECISE BREEDING  
FILE REFERENCE: 058951/0167  
CURRENT APPLICATION NUMBER: US/10/607,538  
CURRENT FILING DATE: 2003-06-27

Query Match	36.6%;	Score 797.6;	DB 19;	Length 1620;
Best Local Similarity	69.3%;	Pred. No. 8.8e-187;		
Matches 1101;	Conservative 0;	Mismatches 484;	Indels 3;	Gaps 1;
Qy	287	TGTTGGATTCTCTAGTGTGCAAACTGCCTTCGTTATCGACATCTGATCAGCTTCTCTGG 346		
Db	11	TGCTGGCTTCTCTGTTTCCAAAACCTGGGCTCTTTGGGTACTTTCAGATCATGCTTCTGTG 70		
Qy	347	TTGCGTTGAATCTCTTTTGTGCACTCTTTGTGCTTGTATGTTCTTTGGTCACTTTTGG 406		
Db	71	TATCCATCAACCTCTTTGTGCACTCTTTGTGCTTGCATCATCATTTGGTCATCTCTTGG 130		
Qy	407	AAGAGATAGATGATGAAGAAATCCATCACCGCTTGTGATTTGGGCTAGGCACTGGT 466		
Db	131	AGGAGAACCGCTGGGTAAATGAGTCCAACTACTGCCCTCATAAATGGTTGTGTACAGAG 190		
Qy	467	TTACCATTTTGTGATTAGTAAAGGAAAAAGCTCGCATCTTCTCGTCTTTAGTGAAGATC 526		
Db	191	TGGTTATCTTGTCTGTAAGTGGTGAAAGAACTCACACCTTCTCGTCTTTCAGTGAAGATC 250		
Qy	527	TTTCTTTCATATATCTTTTGGCACCATTATATTCAATGCAGGGTTTCAAGTAAAAAGA 586		
Db	251	TCCTTTTTCATATATGTACTTCTCCCAATCATATTAAATGCAGGGTTTCAGGTAAAAAGA 310		
Qy	587	AGCAGTTTTTCCGCAATTTCTGTACTATTATGCTTTTTTGGTGTCTTTGGGACTATTATT 646		
Db	311	AGCAATTTTCGTGAACCTTCATTACTATATGATGTTTCGGAGCCATTGGTACCCTGGTCT 370		
Qy	647	CTTGCAAAATCATATCTCTAGTGTGTAAACAGTTCTTTTAAAGATTTGGAACATTTGGAACCT 706		
Db	371	CATGTGCCATTATATCATATTAGTGTGCAATTCAAAATTTTCAAGAACTTTGGAATTTCAATTC 430		
Qy	707	TTGACTTTGGGTGATTATCTTGTCTATTGCTGTCATATTGCTGCAACAGATTTCAGTATGTA 766		
Db	431	TAGATATTGGGATTAICTTTGCAATTTGGAGCAATTTTGTGCCACAGATTTCCGCTGTGCA 490		
Qy	767	CATGCAAGTTCTGAAATCAAGACAGACACCTTTTGTCTTTACAGTCTTTGTAATTCGGAGAG 826		
Db	491	CATTGCAAGTCTTACATCAGATCAGACACCCCTCTTTTACAGTCTTGTATTTCGGAGAAG 550		
Qy	827	GTGTTGTGAATGATGCAACGTCAAGTGTGGTCTTCAAGCGGATTCAGAGCTTTGATCTCA 886		
Db	551	GAGTTGTAATGATGTACATCGGTGTGGTCTTTTCAATGCTATTTCAAAACCTTTGACCTTA 610		
Qy	887	CTCACCTAAAACCAAGAGCTGCTTTTTCATCTTTTGGAAAACCTTCTGTATTGTTTCTCC 946		
Db	611	CGAGCGTGAATCCAGTATAGCCCTCAGTTTCTTTCGGCACTTCTTCTAICTGTCTCTTG 670		
Qy	947	TAAGTACTTGTCTTGGTGTGCAACCGGTCTGATAAGTGCGTATGTTTATCAAGAAGCTAT 1006		
Db	671	CTAGCAGCTTTACTGGGAGCAGGAATCTGGTCTTCTTAGTGTCTAGACTATATCAAGAAGCTGT 730		
Qy	1007	ACTTTGGAAGGCACCTCAACTGACCGAGAGGTGTCCTTATGATCTCTTATGCGGTATCTTT 1066		
Db	731	ATTTTGGCAGGCATCCACAGATCGTGAGGTTGCCCCTTATGATGCTCATGGCTTACTTAT 790		
Qy	1067	CTTATATGCTTGTGAGCTTTTTCAGCTGTAGCGGTATCTTCACTGTGTTTTCTGTGGTA 1126		
Db	791	CATACATCTGGCTGGAATAATTTCTATTGAGTGGGATTTCTCAGTGTATTTTCTGTGGTA 850		

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; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ-ID NOS: 124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-10-369-324-37

```

Query Match 36.5%; Score 794.4; DB 17; Length 1621;  
Best Local Similarity 69.2%; Pred. No. 5.5e-186;  
Matches 1099; Conservative 0; Mismatches 486; Indels 3; Gaps 1;

287	QY	TGTTGGATTCTCTAGTGTGNAAGTCGCTTCGTTTATCGACATCTGATCAGCTTCGTCGTGG	346
11	Db		70
		TGCTGGCTTCTCTGCTTTTCCAAAACGTGGCTCTTTGGGTACTTTCAGATCATGCTTCTCTGTG	
347	QY	TTGCGTTGGAATCTCTTTGTGTGCATCTTCTTTGTGCTTGTTATGTTTCTTTGGTCACTCTTTTGG	406
71	Db		130
		TATCCATCAACCTCTTTTGTGGCACTCCTTTGTGTCTTGCAATCATTTGTCATCTCTTTGG	
407	QY	AAGGAATAGATGATGAAAGAAATCCATCCACCGCTTGTGTGATTTGGGCTAGGCACTGGTG	466
131	Db		190
		AGGAGAAACCGCTGGGTTTAATGAGTCCAAATATCTGCCCTCATAAATTTGGTTTGTGTACAGAG	
467	QY	TTACCATTTTGTGATTAGTAAGAAAGAAAAGCTCGCATCTTCTCGTCTTTAGTGAAGATC	526
191	Db		250
		TGGTTATCTTGCTCGTAAGTGGTGGAAAGAGCTCACACCTTCTGGTTTTCACTGAGATC	
527	QY	TTTCTTCATATATCTTTTGGCCACCCATATATTTCAATGCAAGGTTTCAAAGTAAAAAGA	586
251	Db		310
		TCTTTTTCATATATGTATCTTCTCCAATCATATTTAATGCAAGGTTTTCAGGTAAAAAGA	
587	QY	AGCAGTTTTTCCGAAATTCGTGACTATATGCTTTTTTGGTGTGTTGGGACTATTATTT	646
311	Db		370
		AGCAATTTTTTCGTAAACTTCAATTAATAATGATGTTTCGGAGCCATTTGGTACCCGTGCT	
647	QY	CTTGCACAATCATATCTCTAGGTGTAAACACAGATTTCTTTAAGAAGTTTGGACATTTGGAACCT	706
371	Db		430
		CATGTGCCATTATATCATATTAGTGCCATTCAAACTTTCAAGAAGTTTGGACATTTGAATTC	
707	QY	TTGACTTGGGTGATATCTTGTCATTTGGTGCCATATTTGCTGCAACAGATTCAGTATGTA	766
431	Db		490
		TAGATATTTGGGGATATCTTTGCAATTTGGAGCAATATTTGCTGCCACAGATTTCCGCTCTGCA	
767	QY	CACGTGCAAGTTCGAAATCAAGACAGACACCTTTGCTTTACAGTCTTTGTTATTCGGAGAGG	826
491	Db		550
		CATTTGCAAGTCTTACATCAGGATGAGACACCCCTCTTTACAGTCTTTGATTTGGAGAG	
827	QY	GTGTTTGAATGATGCAACGTCAGTTGTGTGCTTCAACGCGATTCAGAGCTTTGATCTCA	886
551	Db		610
		GAGTTGTAATGATGCTACATCGGTGGTGTCTTTTCAATGCTATTTCAAAACTTCGACCTTA	
887	QY	CTCACCTTAAACCGAAGCTGCTTTTTCATCTTTTGGAACCTTCTCTGTTATTTGTTTCTCC	946
611	Db		670
		CGAGATGAATCCAGTATAGCCCTCAGTTTCTTTGGCAACTCTTCTATCTGTTCCTTG	
947	QY	TAAGTACTTCTGTTGGTGCTGCAACCGGTCGTATAGTGCGTATGTTTATCAAGAAGCTAT	1006
671	Db		730
		CTAGCACTTTACTTGGGAGCAGGAACCTGCTCTTCTTAGTGCTTACATTTCAAGAAGCTAT	
1007	QY	ACTTTTGAAGGCATCAACTGACCGAGAGGTTGGCCCTATGATGCTTTATGGCGTATCTTT	1066
731	Db		790
		ATTTTGGCAGGCACCTCCACAGATCGTGAGGTTGGCCCTTATGATGCTCATGGCTTACTTAT	
1067	QY	CTTATATGCTTGCTGAGCTTTTCCACTTTGAGCGGTATCCTCACCTGTGTTTTTCTGTGGTA	1126
791	Db		850
		CATACTTGTGCGCGAATTTATTTATTTAGTGGGATTTCTCACCGTCTTTTTCTGTGGTA	
1127	QY	TTGTGATGTCCCATTAACATATGGCAAAATGTAAACGGAGAGCTCAAGAATTAACAAAGC	1186
851	Db		910
		TTGTAATGTCTCACTACACTTTGGCAAAATGTAAACGGAGTTCAAGAGTCACTACAAGGC	

; TYPE: DNA			
; ORGANISM: Solanum tuberosum			
US-10-607-538-37			
Query Match		36.5%; Score 794.4; DB 19; Length 1621;	
Best Local Similarity		69.2%; Pred. No. 5.5e-186;	
Matches 1099; Conservative		0; Mismatches 486; Indels 3; Gaps 1;	
QY	287	TGTTGGATCTCTAGTGTGGAACGCTTCGTTATCGACATCTGATCAACGCTTCGTGG	346
DB	11	TGCTGGCTTCTCTGTGTTCCAAACCTGGGCTCTTTGGGTACTTCAGATCATGCTCTGTG	70
QY	347	TTGCGTGTGAATCTCTTTGTGACATCTTTGTGCTTGTATTGTTCTTGGTCATCTTTGG	406
DB	71	TATCAATCAACCTCTTTGTGGCAGCTCTTTGTGCTTGTGATCATCATTTGGTCATCTCTGG	130
QY	407	AAGAGATAGATGATGAACGAATCCATCAGCCCTTGTGATTTGGGCTAGGCACTGGTG	466
DB	131	AGGAGAACCGCTGGGTAAATGATGCTTACTTGCCCTCATATTTGGTTGTGTACAGGAG	190
QY	467	TTACCACTTTTGTGATTAGTAAGAAAGAGTCGTCATCTCTGCTCTTTTGTAGTGAAGATC	526
DB	191	TGGTTATCTTGTCTGAAGTGTGGAAGAGCTCACACCTTCTGCTTTTTCAGTGAAGATC	250
QY	527	TTTTCTTCATATATCTTTTGGCACCATTATATCAATGCAAGGCTTCAAGTAAAGAGA	586
DB	251	TCCTTTTTCATATATGCTCTTCCAAATCATATTTAATGCAAGGCTTTCAGGTAAAGAGA	310
QY	587	AGCAGTTTTCGCGAATTTCTGAGCTATTTATGCTTTTGGTCTGCTTGGGACTATTTATTT	646
DB	311	AGCAATTTTTCGTAACCTTACTTACTATAATGATGTCGGGCACTTGGTACCCTGGTCT	370
QY	647	CTTGACAAATCATATCTCTAGTGTAAACAGCTTCTTTAAGAGTTGACATTTGAACCT	706
DB	371	CATGTGCCATATATCATTTAGGTGCCATTTCAAACTTTCAAGAGTTGGACATTTGAATTC	430
QY	707	TTGACTTGGGTGATTATCTTGCTATTGTTGCCATATTTGCTGCAACAGATTCAGTATGTA	766
DB	431	TAGATATTGGGATTTATCTTGCAATTTGAGCAATATTTGCTGCCACAGATTCGGTCTGCA	490
QY	767	CATCGAGTTCTGATCAAGACGAGACACCTTTTGTCTTTTACAGTCTTGTATTTCGGAGAG	826
DB	491	CATTGCGAGTCTACATCAGGATGAGACACCCCTCTTTTACAGTCTTGTATTTCGGAGA	550
QY	827	GTGTTGTGAATGATGCAAGCTGATTTGGTCTTCAACGCGATTCAGAGCTTTGATCTCA	886
DB	551	GAGTTGTAAATGATGTACATCGGTGGTCTTTTCAATGCTATTCAAACTTCGACCTTA	610
QY	887	CTCAGCTAAACCAAGCTGCTTTTCTATCTTTTGGAACTTCTTGTATTGTTTCTCC	946
DB	611	CGAGATGATATCCAGTATAGCCCTCAGTTTCCCTTGGCACTTCTTCTATCTGTTCCCTG	670
QY	947	TAAGTACCTTGTCTGGTGTCAACCGGTCTGATAAGTCCGTATGTTATCAAGAGCTAT	1006
DB	671	CTAGCACTTTACTGGGAGCAGGAACCTGGTCTTCTTAGTCTTACATTTCAAGAGCTAT	730
QY	1007	ACTTTGGAAGGACCTCAACTGACCGAGAGTTGGCCCTTATGATGCTTATGGGTATCTTT	1066
DB	731	ATTTTGGCAGGCACTCCACAGATCGTGAAGTTGGCCCTTATGATGCTCATGGCTTACTTAT	790
QY	1067	CTTATATGCTCTGAGCTTTTTCGACTTGAAGGCTATCTCACTGTGTTTCTGTGTGTA	1126
DB	791	CATCTTGTGCGCGAATTTATTTCTATTGAGTGGGATTTCTACCGTCTTTTCTGTGTA	850
QY	1127	TTGTGATGTCCATTTACATGCGCAATTTGTAACGAGAGCTTCAAGATAACAAAGC	1186
DB	851	TTGTAATGTCTCACTACACTTGGCACAATGTGACCGAGAGTTCAAGAGTCACTACAAGGC	910
QY	1187	ATACCTTTGCAACTTTTGTCAATTTCTTGGGAGACATTTATTTCTTGTATGTTGAATGG	1246
DB	911	ACACTTTTGGCACTTTGTCAATTTCTTGGCAGAGCTTTCTCTTCTCTATGTGCGCATGG	970
QY	1247	ATGCTTGGACATTTGACAAAGTGGAGATCGTGAAGTGAACACCGGGAACATGATCGCAG	1306

Query Match 35.3%; Score 768.8; DB 21; Length 2330;  
Best Local Similarity 68.6%; Pred. No. 1.5e-179;

RESULT 14  
US-10-944-174-1  
; Sequence 1, Application US/10944174  
; Publication No. US20050032112A1  
; GENERAL INFORMATION:  
; APPLICANT: Fukuda, Atsunori  
; APPLICANT: Tanaka, Yoshiyuki  
; TITLE OF INVENTION: Sodium/Proton Antiporter Gene  
; FILE REFERENCE: SPO-115C1  
; CURRENT APPLICATION NUMBER: US/10/944,174  
; CURRENT FILING DATE: 2004-09-16  
; PRIOR APPLICATION NUMBER: US/09/888,035  
; PRIOR FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: JP 1998-365604  
; PRIOR FILING DATE: 1998-12-22  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2330  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (297)..(1901)  
; OTHER INFORMATION:  
US-10-944-174-1

	Matches	1077;	Conservative	0;	Mismatches	487;	Indels	6;	Gaps	1
Qy	312	GC	TTCGTTATCGACATCTGATACCGCTCTCTGCTGCGTTGGAATCTCTTTGTGCACT	371						
Db	329	GG	CTCTGTACACGACCTCCGACTACGGCTCGGTGGTGTCCATCAACCTGTTCTGTCGCGCT	388						
Qy	372	TC	TTTGTGCTTGTAATTGTTCTTTGGTCACTCTTTTGGAGAGATAGATGGATGAACGAATC	431						
Db	389	GCT	CTGGCCCTGTCATCGTCTCCGCCACCTCCTCGAGGAGAAATCGCTGGGTCAATGATGTC	448						
Qy	432	CAT	CACCGCCTTGTTGATTGGGCTAGGCACATGGTGTACCAATTTGTTGATTAGTAAGG	491						
Db	449	CAT	CACCGCGCTCATCATCGGCTCTGCACCGGCGTGGTGATCTTGCTGATGACCAAGG	508						
Qy	492	AAA	AGCTCGCATCTCTCGTCTTTAGTGAAGATCTTTCTTCATATATCTTTTGCACAC	551						
Db	509	GA	GAGCTCGCACTTATTGCTCTTCAGTGAGATCTCTCTTCATCTACCTCCTCCCTCC	568						
Qy	552	CAT	TATATTCAATCGCAGGTTTCAAGTAATAAAAGAACAGTTTTTCGCGAATTTCTGTGAC	611						
Db	569	GAT	CATCTTCAATCGAGTTTTTCAGGTAAGAAAAAGCAATTTCTTCGGGAATTTTCATGC	628						
Qy	612	TAT	TATGCTTTTGGTCTGTGGGACTATTATTCTTTGGCACATCATATCTCTAGTGT	671						
Db	629	GAT	CACAAATTATTGGAGCGTGGGCAATGATATCTTTTTCACAATATCTATTGTCTG	688						
Qy	672	AA	CACTCTTTAAGAAGTTGGACATTTGGAACCTTTTGACTTGGGTGATATTCTTGCTAT	731						
Db	689	CAT	TGCAATATTACGAGAATGAACATTTGGNACGCTGGATGAGGAGATTTCTTGCAAT	748						
Qy	732	TGG	TGCCAATATTGCTCGCAACAGATTCAAGTATGATGACATGCGAGTTTCTGAATCAAGACGA	791						
Db	749	TGA	GCCATCTTTTCTCGCACAGATTTCTGTCTGCACATGCGAGTCTCTCAATCAGGATGA	808						
Qy	792	GAC	ACCTTTGCTTTACAGTCTTGATTTGGGAGGGTGTGTGAATGATGCAAGTCACTCAGT	851						
Db	809	GAC	ACCTTTTGTGACAGTCTGGTATTTCGGTGAAGGTGTTGTGAACGATGCTACATCAAT	869						
Qy	852	TGT	TGCTTCTCAACCGCATTCAGAGCTTTGATCTCACTCACCTAAACACCAAGCTGCTTT	911						
Db	869	TGT	GCTTTTCAACGCACTACAGAACTTTGATCTTGTCACATAGATGCGGCTGTCGTTCT	928						
Qy	912	TC	ATCTTCTTGGAAACTTCTTGTAATTTGTTTCTCCTAAGTACCTTGTTGGTGTCTGCAAC	971						
Db	929	GAA	ATTCTTGGGAACTCTTTTATTATTATTTTTGTGAGCACCTTCTCTGGAGTATTGTC	988						
Qy	972	CG	GTCTGATAAGTCCGTATGTTATCAGAAGCTATATCTTTGGAAGGCACCTCACTGACCG	1031						
Db	989	TGA	TTGCTCAGTGCATACATAATCAAGAAGCTATACATTGGAAGGCATTTCTACTGACCG	1048						
Qy	1032	AGA	GTGCCCCTATGATGCTTATGGCGTATCTTTCTTATATGCTCTCGAGCTTTTCGA	1091						
Db	1049	TGA	GTGCCCCTTANGATGCTATGGCTTACCTTTTCATATATGCTGGCTGAGTTGCTAGA	1108						
Qy	1092	CTT	GACGGTATCCTCACTGTGTTTTTCTGTGGTATTGTGATGTCCCATTTACACATGGCA	1151						
Db	1109	TTT	GACGGCATTCCTCACCGATTTCTTCTGTGGTATTGTAATGTCACTTACACTTGGCA	1168						
Qy	1152	CA	ATGTAAACGAGAGCTCAAGATAACAAACAAAGCATACCTTTTGCAACTTTGTGATTTCT	1211						
Db	1169	TA	ACGTACAGAGAGTTCAAGAGTACAACAAAGCACGCAATTTTGCAACTCTGTCTTTTCA	1228						
Qy	1212	TGG	GAGACATTTATTTTCTTTGATGTTGGAATGGATGGCTTGACATTCGAAGTGGAG	1271						
Db	1229	TGT	TGACATTTCTTCTGTATGTTGGATGGATGGATTTGGATATTGAAATATGGGA	1288						
Qy	1272	AT	CCGTGAGTGACACACCGGAAACATCGATCGCAGTGAGCTCAATCCCTAATGGGTCTGGT	1331						
Db	1289	GTT	TGCCAGTGACAGACCTCGCAATCCATTGGGATAAGCTCAATTTTGTAGGATTTGGT	1348						
Qy	1332	CAT	GTTGGGAAGAGACGGTTTGTCTTTTCCGTTATTCGTTTCTATCTAACTTAGCCAAAGAA	1391						
Db	1349	TC	GATTGGAAGAGCTGCTTTGTATTTCGCGCTGCTGCTTTCTGTGCGAACCTTAAACAAAGAA	1408						

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RESULT 15
US-10-155-535-3
; Sequence 3, Application US/10155535
; Publication No. US20030046729A1
; GENERAL INFORMATION:
; APPLICANT: Blumwald, Eduardo
; APPLICANT: Apsee, Maris
; TITLE OF INVENTION: EXPRESSION OF VACUOLAR CATION-PROTON ANTI-PORTERS
; TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY
; EXPRESSION OF VACUOLAR CATION-PROTON ANTI-PORTERS
; FILE REFERENCE: 529152000720
; CURRENT APPLICATION NUMBER: US/10/155,535
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 09/271,584
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,474
; PRIOR FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: 60/116,111
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2066
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-155-535-3

Query Match      33.0%; Score 719; DB 14; Length 2066;
Best Local Similarity 66.0%; Pred. No. 3.le-167;
Matches 1056; Conservative 0; Mismatches 540; Indels 3; Gaps 1;

QY      326  CATCTGATCACGCTTCTGTGGTTCGATCTTTTGTGACATCTTTTGTGCTTCTTTGTGCTTGA 385
Db       50  CTTCTGATCATGATCGGTCGTCTCCATGAATTTGTTCTAGCTTTGTGCTTGA 109
Ov      386  TTGTCTTGTGTCATCTTTTGGAAAGAGAATAGATGATGAACGAATCCATCACCGCCTTCT 445

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Db	110	TCGTCGCTGGTCACTGCTTGAGGAGACTCGGTGGATGGAACGAGTCAATCACTGCCTCTTA	169
Qy	446	TGATTGGCGTAGGCACCTGGGTGTACCAATTTGTTGATTAGTAAAGGAAAAAGCTCGCATC	505
Db	170	TCATTGGTTCGTGTACTGGGTTGTGATCTTGCTTATTAAGTGGNGGCAAGGCTCAAGGA	229
Qy	506	TTTCGCTCTTTAGTGAAGATCTTTTCTTCATATATCTTTTGGCCACCATTATATTCAAATG	565
Db	230	TTCTTGTTGTAGTGAAGATCTCTCTCTTTATTTATCTTCTCCACCAATATATTTCAACG	289
Qy	566	CAGGGTTTCAAGTAAAAAAGAGCAGTTTTTCCGCAATTTTCGTGACATTTATATGCTTTTGG	625
Db	290	CAGGGTTTCAGGTTAAGAAGAAGCAATTTTTTTCGCAACTTCATGACCAATATGTTATTTG	349
Qy	626	GTGCTGTTGGGACTATTTATTTCTTGCAAAATCATATCTCTAGGTGTAAACAGTTCTTTTA	685
Db	350	GTGCTATTGGAACTCTCATTTTCATTTGTGTATCATCTCATTTGGTGTAAACATCTTTTCG	409
Qy	686	AGAAATGGACATTTGGAACTTTGACTTGGGTGATATCTTGCTATTGGTGGCCATATTTG	745
Db	410	AGAAATGAAATATCGGTGATCTTACCATTTGCGGACTATCTAGCCATTTGGAGCAATATCT	469
Qy	746	CTGCAACAGATTCAGTATGTACATCGAGGTTCTGAATCAAGACGAGACACCTTTGCTTT	805
Db	470	CTGCTACAGACTCTGTTTGGCACTTGCAGTGTCAATCAAGACGAGACACCTCTCTGTGT	529
Qy	806	ACAGTCTTGATTCGGAGAGGGTCTCTGAATGATGCAACGTCAGTTGTGCTCTTCAACG	865
Db	530	ACAGTCTTGCTTTGGAGAGGGTGTAGTGAAAGATGCCATCGTCTGCTCTTCAATG	589
Qy	866	CGATTCAGAGCTTTGATCTCACTCACCTAAACACGAGGCTGCTTTTTCATCTCTCTGAA	925
Db	590	CAATACAGAGATTCGACCTCACAAATATCAATTCAGCCATAGCTTTGGAGTTTGCCTGAA	649
Qy	926	ACTTCTTGATTTGTTTCTCTAAGTACCTTGTGTGTGTCTGCAACCGGTCTCATTAAGTG	985
Db	650	ACTTTTTTTTACCTCTTTTATCTTAAGCACAGCAGCTTGTGTGTGCACTGGAATGCTCAGTG	709
Qy	986	CGTATGTTATCAAGAAGCTATCTTTCGAAGGCACCTCACTGACCGAGAGGTTGCCCTTA	1045
Db	710	CTTTTGTTATCAAGAGCTCTATATAGGAAGGCCACTCTACTGATCGTGAAGTTGCACTTA	769
Qy	1046	TGATGCTTATGGCGTATCTTTCTTATATGCTTGTCTGAGCTTTTCGACTTGAGCGGTATCC	1105
Db	770	TGATGCTATTGGCTTACTTATCATATATGTTGSCAGAGCTATTCACCTTCGAGCTCTATCT	829
Qy	1106	TCAGTGTGTTTTCTGTGGTATTGTGATGTCCCATTAACATGGCACAATGTTAACGGAGA	1165
Db	830	TGACTGTGTTCTTCTGCGGATTTGTTATGTCTCACTATACATGGCACAATGTTACAGATA	889
Qy	1166	GCTCAAGAAATAACAAGACATACCTTTCGCACTTGTCTCATTTCTTTCGCGAGACATTTTA	1225
Db	890	AATCCAAGTCACTACAAAACATACTTTTGTGCAATGTCTTCTAGCTTGAGATTTTTTA	949
Qy	1226	TTTTTCTTGATTTGGAAATGGATGCCCTTGACATTTGAAGTGGAGATCCGTCAGTGACA	1285
Db	950	TCITTCTTTACGTTTGGAAATGGAAGCTCTCGATATCGAGAAATGGGAGTTGTACGCAACA	1009
Qy	1286	CACCGGAAACATCGATCGCAGTAGCTCAATCTTAATGGGTCTGGTCTATGGTTGGAAAGAG	1345
Db	1010	GTCCTGGTCAGTCGATTGGAGTTAGTTCAATACTTCTTGGGCTTATTTCTTCTGGGTCCGC	1069
Qy	1346	CAGGGTTCGTTTCCGTTATCGTTTCTATCTAACTTTAGCCAGCAAGAAATCAAGCGAGA	1405
Db	1070	CCGGTTCGTTTTTCCACTTTCTCTCTGTGTCCAATTTTAAACAGTCTTCCACCGATGAGA	1129
Qy	1406	AAATCAACTTTAAACATGCAGGTTGTGATTTGGTGGTCTGCTCTCATGAGAGGTGCTGTAT	1465
Db	1130	AAATAGACTTTAAGAAACAGTAACCAATTTGGTGGGCTGGTCTGATCGGTGGTGCATGT	1189
Qy	1466	CTATGGCTCTTGCAACAACAAGTTTACAAGGCCGGGCAACACAGATGTATCGCGGAATG	1525

Db	1190	CAATGGCTCTTGCTTATAACCGATTCAACAATCTTCAGGACACACC	AAAGTTCTTTGGGAACG	1249
Qy	1526	CAATCATGATCACGAGTACGATAAATGTCTGTCTTTTATAGCACAGT	GTGTTTGGTATGC	1585
Db	1250	CTATCATGATCACAGTACCATCATCTGTTGTCTTTTCAGTACTG	GGTGTTCGATTCG	1309
Qy	1586	TGACCAAAACCACTCATAAAGTACTATTACCGCACAGAACGCGCAC	ACGAGCATGTTAT	1645
Db	1310	TAACCAAAACGGTTAGTCAAAACATTTGACGGCTTCATAAAACAGT	CCTCCACGACCGCGC	1369
Qy	1646	CTGATGACAAACCCCAAAATCATATATCCCTTTGTTGGACCAAGACT	CGTTCATTG	1705
Db	1370	TGCAGATCACACTAAGATCTTCTTTCCAGATCCGATCCTCCATGAG	CGCTTGCTCAGTA	1429
Qy	1706	AGCCTTCAGGGAACCAATGTGCCT--CGGCGCTGCACAGTATACGT	GCGTCTTGACAC	1762
Db	1430	CCCAAGCCAGTCAGAATACGACCTGAAACAACATGTTAGCTTCAGA	ATGTTCTCGAAAT	1489
Qy	1763	GGCCCACTCGAACGGTGCAATTACTCTGGAGACAAATTTGATGACT	CTTCATCGGACCCG	1822
Db	1490	CTCCGTCCAGGGCAATTCATCATTTACTTGGAGGAAATTCGATAAC	GCAAGTTATCGCTCGCA	1549
Qy	1823	TCTTTGGAGTCTGTGGCTTTGTACCCCTTTGTTCCAGGTTCTCCA	ACTTGAGAGAACCCCTC	1882
Db	1550	TATTTGTTGGCCGAGGCGTTTCCACCAAGTAGTTCCAGGTTCA	CCCATTTGAGAAATAGTGTTTC	1609
Qy	1983	CTGATCTTAGTAAGCTTTGAGGGTAACTGGAAGAAAG		1921
Db	1610	CGCAATGGAGTGAAGAAGTAGAAACCAAGGAACAAACG		1648

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Job time : 1444 secs

GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 28, 2005, 02:15:26 ; Search time 377 Seconds  
(without alignments)  
9453.079 Million cell updates/sec

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Perfect score: 2178  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	821.2	37.7	2553	US-09-830-123-16	Sequence 16, Appl
2	813	37.3	2423	US-09-830-123-14	Sequence 14, Appl
3	774.8	35.6	2237	US-09-830-123-1	Sequence 1, Appl
4	754.4	34.6	2361	US-09-830-123-18	Sequence 18, Appl
5	91.2	4.2	1581	US-09-800-729-22	Sequence 22, Appl
6	64.4	3.0	1354	US-09-800-729-58	Sequence 58, Appl
7	64.4	3.0	1688	US-09-800-729-57	Sequence 57, Appl
8	60.6	2.8	4452	US-09-949-016-849	Sequence 849, Appl
9	59.8	2.7	4460	US-09-949-016-4129	Sequence 4129, Appl
10	53.8	2.5	1291	US-09-524-101D-5	Sequence 5, Appl
11	53.8	2.5	2007	US-08-747-221B-36	Sequence 36, Appl
12	53.8	2.5	2007	US-08-747-221B-38	Sequence 38, Appl
13	53.8	2.5	2007	US-09-005-051-36	Sequence 36, Appl
14	53.8	2.5	2007	US-09-005-051-38	Sequence 38, Appl
15	53.8	2.5	2007	US-09-403-942F-36	Sequence 36, Appl
16	53.8	2.5	2007	US-09-403-942F-38	Sequence 38, Appl
17	53.6	2.5	17612	US-09-949-016-15061	Sequence 15061, A
18	50	2.3	1141	US-09-806-708B-22	Sequence 22, Appl
19	48.8	2.2	1169	US-09-100-391-5	Sequence 5, Appl
20	48.8	2.2	1169	US-09-616-614-5	Sequence 5, Appl
21	48.8	2.2	1302	US-09-100-391-11	Sequence 11, Appl
22	48.8	2.2	1302	US-09-616-614-11	Sequence 11, Appl
23	48.8	2.2	2643	US-09-100-391-9	Sequence 9, Appl
24	48.8	2.2	2643	US-09-616-614-9	Sequence 9, Appl
25	48.4	2.2	684	US-09-248-796A-6653	Sequence 6653, Appl
26	48.4	2.2	1664976	US-08-916-421B-1	Sequence 1, Appl
27	48.4	2.2	1664976	US-09-692-570-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

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US-09-830-123-16
; Sequence 16, Application US/09830123
; Patent No. 6803500
; GENERAL INFORMATION:
; APPLICANT: Iida, Shigeru
; APPLICANT: Tanaka, Sachiko
; APPLICANT: Inagaki, Yoshishige
; TITLE OF INVENTION: Genes Encoding Proteins Regulating the pH of Vacuoles
; FILE REFERENCE: 001560-397
; CURRENT APPLICATION NUMBER: US/09/830,123
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: PCT/JP00/05722
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: JP 11/236800
; PRIOR FILING DATE: 1999-08-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 16
; LENGTH: 2553
; TYPE: DNA
; ORGANISM: Nierebergia hybrida
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2553)
; OTHER INFORMATION: Nucleotide sequence of DNA encoding for protein regulating the
; OTHER INFORMATION: pH of vacuoles
US-09-830-123-16

Query Match          37.7%; Score 821.2; DB 4; Length 2553;
Best Local Similarity 70.3%; Pred. NO. 2e+199;
Matches 1115; Conservative 0; Mismatches 468; Indels 3; Gaps 1;

QY 289 TTGGATTCTCTAGTGTCCAACTGCTTCGTTATCGACATCTGATCAGCTTCTCTGGTT 348
Db 543 TTGGGATCTGCTGGGAAAGATGAACAACTTCTGATCATCAATCACTGGTG 602
QY 349 GCGTTGAATCTCTTTGTTGCACATCTTTGTTGCTGTATTTGTTCTTGGTTCATCTTTGGAA 408
Db 603 TCGGTAAACTTTGTTGTCATTTATTTGCGGTGTTGTTGATCGGTTCATTTATTTGGAG 662
QY 409 GAGATAGATGATGAAGCAATCCATCACCGCTTTGTTGTTGGCTAGGCACTGGTGT 468
Db 663 GAAACAGATGATGAATGAGTCCATACTGCCCTTGTGTTGGTAGTTGCACTGGAGTC 722
QY 469 ACCATTTTGTGTTAGTAAAGGAAAGCTCGGATCTTCTCGTCTTTAGTGAAGATCTT 528
Db 723 ATCATTTTACTAATAAGTGGAGAAAGAACACATATTTTAGTGTTCAGGGAAGATCTT 782
QY 529 TTCTTCATATATCTTTTCCACCCCATTTATTTCAATGCGAGGTTTCAAGTAAAAAAGAG 588
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D	b		TTCCTCATTACCTTCTCCACCAGCATATTTTAATGCTGGGTCCAGGTGA AAAAAGAAA	842
Q	y		CAGTTTTTCCGCAATTTCTGACTATTATGCTTTTCTGCTGCTGTGGGACTATTATTCT	648
D	b		TCATTTCTCCGCAATTTTCAGTACTATCATGCTCTTTGGGGCAGTTGGCACCTTGATATCG	902
Q	y		TGCACAATCATATCTCTAGGTGTAAACACAGTTCTTTAAGAAGTTGGACATTTGAACCTTT	708
D	b		TTCATTTATATATCAGCGGTGCTATTGGCATTTTCAAGAAATGGATATTGGACACCTT	962
Q	y		GACTTGGGTGATATTCTTGTCTATTGTGGTGCCATATTCTGCTGCAACAGATTCAGTATGTACA	768
D	b		GAATAITGGAGATTACCTTTGCCAATTTGGAGCAATCTTTGCTGCAACAGATTCGTATGCACC	1022
Q	y		CTGCAGGTTCTGAATCAAGACGACACCTTTGCTTTTACAGTCTTGTTATTCGGAGAGGT	828
D	b		TTACAAGTGCTTAATCAGGAAGAACACCGTTATTGTACAGTCTAGTGTGTTGGAGAAGGT	1082
Q	y		GTTGTGAATGATGCAACGCTCAGTTGTGCTCTTCAAACGCAATCAGAGCTTTGATCTCACCT	888
D	b		GTTGTGAATGATGCCACATCTGTAGTCTGTTCAATGCTGCTCCAGAATTTGACTTATCT	1142
Q	y		CACCTAAACCAAGAGCTGCTTTTCATCTCTTTGGAAAACTTCTTGTAATTTGTTTCTCCCTA	948
D	b		CATATCAGCACAGGCAAAAGCTCTGCAATTAATTGAAAACTTTCTATACTTGTGTTGCCCTG	1202
Q	y		AGTACTTCTGCTGTGCTGTCGAACCGGTCTGATAGTGGGTATGTTATCAAGAGCTATAC	1008
D	b		AGCACTTCTTAGGGTGTCTGTGGCTACTAAGTGCCCTTATAATTAAGAACTCTAC	1262
Q	y		TTTGGAAAGCACTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGGCGTATCTTTCT	1068
D	b		TTTGGAGGCACCTCGACTGTCGTGAGGTTGCTATATGATACTCATGGSGTACCTATCA	1322
Q	y		TATATGCTTGTGAGCTTTTTCGACTTGAGCGGTATCTCTACTGTGTTTTTCTGTGTPATT	1128
D	b		TACATGCTTGTGTAATTAATCTATTTAAGTGGAACTCTCACTGTGTTTTTCTGTGGGATC	1382
Q	y		GTGATGTCCCAATTACATGSCACAAATGAACGAGAGACTCAAGATAACAACAAGCAT	1188
D	b		GTGATGTCTCACTATACCTGGCAATAATGTGACTGAGAGCTCAAGAGTCACTACAAGCAC	1442
Q	y		ACCTTTGCACCTTGTCTATTCTTTCCGAGACATTTATTTTCTTGATGTGGAAATGGAT	1248
D	b		ACGTTTGTCTACATTAATTTTGTCTGAAATTTCTATATCTCTTATGTGTTGTTATGAT	1502
Q	y		GCCTTGGACATFTGACAGTGAGAGATCCGTGAGTGACACACGGGAAACATCGATCGCAGTG	1308
D	b		GCCTTGGACATTTGAGAAGTGGAGTTTGTAAAGCGACAGCCCCGGAAACATCAATTAAGTTC	1562
Q	y		AGCTCAATCTTAATGGGCTCGGTCACTGGTTGGAGAGACAGGTTCTGTTTCCGTTATCG	1368
D	b		AGCTCAATCTTGTAGGTCTGTGTTTGGTTGGAAAGGGGAGCCCTTGTGTTTCCCCTTGTCA	1622
Q	y		TTTCTATCTAACTTAGCCAAGAAATCAAAAGCGAGAAATCAACTTTTAACATCGAGGTT	1428
D	b		TTCTGTGTCCAACTTGACCAAGMAAANTCTTGAGGACAAGATTAGCTTTAACACGAGGTT	1682
Q	y		GTGATTTGGTGGTCTGCTCATGAGAGGTGCTGTATCTATGGCTCTTGTCATACAACAG	1488
D	b		ACAATAATGGTGGGCTGGGCTTATCGCAGGTGCTGTTTCTATGGCCCTTGCTTATAATCAG	1742
Q	y		TTTACAAGGCCGGGCACACAGATGTACGGGGNAATGCAATCATGATCAAGAGTACGATA	1548
D	b		TTTACCAGGGGAGGTCTATCTCAGTACGTGCCAATGCAATAATGATCAGGAGTACTATC	1802
Q	y		ACTGCTGTCTTTTATGACAGAGTGGTGTGTTGGTATGCTGACCAAAACC--ACTCAATAGC	1605
D	b		ACTGTTGTCCTTTTTCAGCANCGTGGTATTTGGGTTGATGACAAAACCTTTAATCTTATTA	1862
Q	y		TACCTATTACCGCACCAAGAACCGCCACCAGAGCATGTTATCTGATGACAAACCCCAAAA	1665

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RESULT 2
US-09-830-123-14
; Sequence 14, Application US/09830123
; Patent No. 6803500
; GENERAL INFORMATION:
; APPLICANT: Iida, Shigeru
; APPLICANT: Tanaka, Sachiko
; APPLICANT: Inagaki, Yoshishige
; TITLE OF INVENTION: Genes Encoding Proteins Regulating the pH of Vacuoles
; FILE REFERENCE: 001560-397
; CURRENT APPLICATION NUMBER: US/09/830,123
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: PCT/JP00/05722
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: JP 11/236800
; PRIOR FILING DATE: 1999-08-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 2423
; TYPE: DNA
; ORGANISM: Petunia hybrida
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(2423)
; OTHER INFORMATION: Nucleotide sequence of DNA encoding for protein regulating the
; OTHER INFORMATION: pH of vacuoles
US-09-830-123-14

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Query Match	37.3%;	Score 813;	DB 4;	Length 2423;
Best Local Similarity	70.6%;	Pred. No. 2.5e-197;		
Matches 1099;	Conservative 0;	Mismatches 455;	Indels 3;	Gaps 1;
Qy	318	GTTATCGACATCTGATCAGCTTCTGTGGTTGGTTGGAATCTCTTTTGTGCACTTCTTTG	377	
Db	393	GTTATCGACATCTGATCATCAATCAGTTGTGTCGATAAACTTATTCTGTTGCTCTTATTG	452	
Qy	378	TGCTCTGATTGTTCTTTGGTTCATCTTTTGGAAAGAAATAGATGATGATCAAGCAATCCATCAC	437	
Db	453	CGCGTGATTGTGATCGGTCAITTTGTGGAAGAAAACAGATGATGATGAATGATCCATAAC	512	
Qy	438	CGCTTTGTTGATTGGCTAGGCACCTGGTGTTACCATTTTGTGATTAGTAAAGGAAAAAG	497	
Db	513	TGCTTTAGTGTGTTCTTGTTACTGGAATCGTTATTCTACTGATAAGTGGAGGAAAAAGAA	572	
Qy	498	CTCGCATCTTCTCGTCTTTAGTGAAGATCTTTTCTTCATATATCTTTTGGCCACCCATTAT	557	
Db	573	CTCTCATATTTTAGTGTTCAGTGAAGATCTTTTCTTCATTACCTTCTTCCGCGCAATCAT	632	
Qy	558	ATTCAATGCAGGGTTTCAAGTAAAAAGAGCAGTTTTTCCGCAATTTCTGTGACTATTAT	617	
Db	633	TTTTAATGCTGGGTTCCAGTGAAGAAAGAAATCGTTCTTCCGCAATTTGACGACTATTCAT	692	
Qy	618	GCTTTTTGGTGTGTTGGGACTATTATTTCTTGGCAACAATCATATCTCTAGGTGTAACACA	677	

Db 693 GCTCTTTGGGCACTTGGCACCTTGATATCATTTATTTATCATTTAGTGCCATTGG 752  
Qy 678 GTTCTTTAAGAAAGTTGGACATTTGGAACTTTTGCATTTGGGTGATTTCTTTGTTGTTGTC 737  
Db 753 CATTTTCAAGAAATGAATTTTGAAGCCCTTGAATTTGAGATTTACCTTTGCATTTGGGTC 812  
Qy 738 CATATTTGCTCAACAGATTTCAAGTATGTAACCTGCAAGTTTCTGAATCAAGACGACACCC 797  
Db 813 AATCTTCTCTGCTACAGATTTCTGATGCACTTTCAAGTGTCTTAATCAGGATGAACACC 872  
Qy 798 TTTGCTTTACAGTCTTGTATTCGGAGAGGGTGTGTGAATGATGCAACGTCAGTTGTGGT 857  
Db 873 CTTATTTGACAGTCTAGTTTGTGGGGAAGGTGTGTGAATGATGCAACATCTGTATTTCT 932  
Qy 858 CTTCAACGGGATTCAGAGCTTTGATCTCACTCACTAAACACGAAAGCTGCTTTTCATCT 917  
Db 933 GTTCAATGCTATCCAGAACTTTGACTTATCTCAATCGACACGGGAAGCTATGGAAT 992  
Qy 918 TCTTGGAACTTCTTGTATTTGTTTCTCTAAGTACCTTTGCTTGTGCTGCAACCGGTCT 977  
Db 993 AGTTGGAACTTCTTATATCTTTTGGCTCAAGCACTGCCCTAGGAGTTGCTGTGGCT 1052  
Qy 978 GATAAGTGGGTATTTCAAGAACTATATCTTTGGAAGGCACTCAACTGACCGAGAGGT 1037  
Db 1053 ACTGAGCGCTATATTTTAAAGAACTCTACTTTTGAAGGCACTCAACTGACCGGTGAGGT 1112  
Qy 1038 TGCCCTTATGCTTATGGGCTATCTTTCTTATATGCTGTGAGCTTTTTCGACTGAG 1097  
Db 1113 TGCTATATGATACCTATGCTGCTTCTTATCTTCAATGCTTGTGATTTATTTAAG 1172  
Qy 1098 CGGTATCTCTCACTGTGTTTCTGTGTTATGTTGATGTGCCATTTACATGCGCAATGT 1157  
Db 1173 TGCAATCTCTCACTGTGTTTCTCTGGGATGCTGATGCTCACTACACTGGCATAATGT 1232  
Qy 1158 AACGAGAGCTCAAGAAATACAAAGATACCTTTTGAACCTTTGTCATTTCTTGGGA 1217  
Db 1233 GACTGAGAGCTCGAGAGTCACTTACCAGCACTTTTGTCTACATTTATTTATTTGCTGA 1292  
Qy 1218 GACATTTATTTCTTGTATTTGGAATGATGCTTGTGACATTTGACAAAGTGGAGATCGT 1277  
Db 1293 AATATTCATTTCTTATTTGTTGATGATGCTTGTGACATTTGAGAGTGAAGTTGT 1352  
Qy 1278 GAGTGACACACCGGAAACATCGATCGAGTGAAGTCAATCTTAATGGGTCTGGTCATGGT 1337  
Db 1353 AAGCCAGAGCTGGAATATCAGTTTCAAGTTAGCTCAATATTTGCTGGTCTTTGTTGTT 1412  
Qy 1338 TGGAAGAGAGGTTTGGTCTTTCCTGTTATCGTTTCTATCTAATCTTAGCCAAAGAAATCA 1397  
Db 1413 TGGAAGAGAGCATTTGTTTCCCATTTGTCTTGTCTCAACTTTGACCAAGAAACTCC 1472  
Qy 1398 AAGCCAGAAATCAACTTTTACATCGAGTTGTGATTTGGTGTCTGCTCATGAGAGG 1457  
Db 1473 AGAGCGGAAATAGTTTAAACAGAGGTTACAAATATGGTGGCTGGACATTTAGAGAGG 1532  
Qy 1458 TGCTGTATCTATGGCTTTTGCATACAAAGTTTACAAAGGCGCGGACACAGATGTACG 1517  
Db 1533 TGCCGTCTTATGGCCCTTGTCTTAATCAAGTTTACAGGGGAGGTCTACTCAGTTAGG 1592  
Qy 1518 CGGGAATGCAATCATGATCAAGTACGATTAATCTGTCTGTCTTTTATAGACAGTGGTGT 1577  
Db 1593 CGCAATGCAATTAATGATCAAGTACTATCACTGTCTGTCTTTTTCAGCAGAGTGGTGT 1652  
Qy 1578 TGATATGCTGACCAACCACTCAT--AAGCTACCTTATACCGCACCAAGACGCCACCAC 1634  
Db 1653 TGAGGTGATGACAAACCTTTGATTTAGAAATATGTACCTTACACAAACACTTTGAGCAG 1712  
Qy 1635 GAGCATGTTATCTGATGACAAACACCCCAAAATCCATATATATCTTGTGTGGACCAAGA 1694  
Db 1713 AATGATCTTCTGAAACCAACGACCCCAAAATCTTCAATTTGTCACACTTCTTGACAGC 1772  
Qy 1695 CTCGTTCAATGAGCTTCAGGGAACCAATATGTGCTCGGCTGACAGTATACGTTGCTT 1754

Db 1773 ACAAGACTCAGAAGCTGATCTGGAAAGCCATGTATACCCGTCGCCACAGTTTTCGGATGCT 1832  
Qy 1755 CTTGACACGGCCCACTCGAACCGTGCAATTACTACTGGAGACAAATTTGATGACTCTCTTCAT 1814  
Db 1833 CTTTCAACCCATCTCATACAGTCAATTTACTGGAGAAAGTTTGCAATGCAATTCAT 1892  
Qy 1815 GCGACCCGCTTTTGGAGGTCTGGCTTTGTACCCCTTTGTTCCAGGTTCTTCCAACTGA 1871  
Db 1893 GCGTCCAGTTTTCGGTGGACGAGGTTTGTACCTTTTGTCTCCAGGATCACCGACAGA 1949

RESULT 3  
US-09-830-123-1  
; Sequence 1, Application US/09830123  
; Patent No. 6803500  
; GENERAL INFORMATION:  
; APPLICANT: Iida, Shigeru  
; APPLICANT: Tanaka, Sachiko  
; APPLICANT: Inagaki, Yoshihide  
; TITLE OF INVENTION: Genes Encoding Proteins Regulating the pH of Vacuoles  
; FILE REFERENCE: 001560-397  
; CURRENT APPLICATION NUMBER: US/09/830.123  
; CURRENT FILING DATE: 2001-04-24  
; PRIOR APPLICATION NUMBER: PCT/JP00/05722  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: JP 11/236800  
; PRIOR FILING DATE: 1999-08-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2237  
; TYPE: DNA  
; ORGANISM: Ipomoea nil  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(2237)  
; OTHER INFORMATION: Nucleotide sequence of DNA encoding for protein regulating the  
; OTHER INFORMATION: pH of vacuoles  
US-09-830-123-1

Query Match 35.6%; Score 774.8; DB 4; Length 2237;  
Best Local Similarity 69.2%; Pred. No. 1.3e-187;  
Matches 1096; Conservative 0; Mismatches 467; Indels 21; Gaps 2;  
Qy 319 TTATCGACATCTGATCAGCTTCTGCTTCCGTTTGAATCTCTTTGTTGCACTTCTTTGT 378  
Db 339 TTGTTACGCTGATCATGCTTCCGTTGTGCTGATGAACCTCTTTTGGCGGTGCTTGGC 398  
Qy 379 GCTTGTATTTGTTTGTGTCATCTTTTGGAGAGAAATAGATGGATGAACGAATCCATCACC 438  
Db 399 GCATGCATTTGTTCTTGGCCATCTACTCGAGGAGAAATCGCTGGTGAACGAATCCATTACT 458  
Qy 439 GCCTTGTGATTTGGCTAGGCATCTGGTTTACCAATTTTGTGATTTAGTAAAGGAAAGAC 498  
Db 459 GCCCTTAATTTGTTTGTGCACCGAGTTGTAAATTTTGTCTTCTTAGCGGAGAAAGAGT 518  
Qy 499 TCGCATCTTCTCGCTTTTAGTGAAGAGCTTTTCTTCTATATATCTTTTCCACCCCAATTATA 558  
Db 519 TCACATCTTCTGCTTTTAGCGAAGATCTTTCTTATATATCTCTGCGCACCTTATATA 578  
Qy 559 TTCAATCGAGGGTTTCAAGTAAAAAAGACAGATTTTTCGCAATTTTCGTCGACTATTATG 618  
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Qy 619 CTTTTTGGTGTCTGTTGGGACTATTTATTTCTTTCGCAATCATATCTTAGGTGTAAACACAG 678  
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Qy 679 TTTTAAAGAGTTGGACATTTGGAACCTTTTCTGCTTGGTGTATTTCTTGTCTATTGTTGCC 738  
Db 699 ATTTTCAAGCACTTAGACATTTGACTTTCTGGAATTTTGGAGATTTATTAGCAATTTGGTGG 758  
Qy 739 ATATTTGTCACACAGATTTTCAAGTATGTATGTAACACTGCGAGTTTCTGAAATCAAGACGAC 798

Db 759 ATATTGTGCAACCGATCTGTTTGCACATTCAGAGTGTCTCAGTCAGATGAGACGCC 818  
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Qy 859 TTCAACGGCATTCAGAGCTTTGATCTCACTCACTCACTAAACCGAAGCTGCTTTTCATCTT 918  
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Qy 979 ATAAAGTGGTATGTTATCAAGAAGCTATATCTTTTGAAGCACTCAACTGACCGGAGGTT 1038  
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Qy 1039 GCCCTTATGATGCTTATGGCGTATCTTTCTTATATGCTTGTGAGCTTTTCGACTTGAGC 1098  
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Qy 1159 ACGGAGAGCTCAAGAATCAACAAGCATACCTTTTGCACTTTGTCTATTTCTTTGCGGAG 1218  
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Db 1359 GGCAGAGCTGGGTTGCTATTCCTCTGTTGCTTTTATCCAACTTAGCAAGAAACTCT 1418  
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Qy 1519 GGGAAATCAATGATCAAGTACGATACGATATCTGTCTGTTTATGTTTATGACAGTGGTGT 1578  
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Qy 1579 GGTATGTCGACCAACCACTCATAGCTACTATTACCGACACAGACCGCACCAAGC 1638  
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Qy 1693 TTTGACCAA-----GACTCGTTCAATGAGCCCTTCAGGGAACCAATATGCGCTCGGCT 1737  
Db 1719 CTGGACAAACCAACCTGACTCAGAAAGCGATATGATAACCGGACCTGAGGTTGCTCGACCA 1778  
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Qy 1798 TTTGATGACTCTCTTATCGACCGCCGCTCTTTGGAGGTCTGTGGCTTTGTACCCCTTTGTTCCA 1857

Db 1839 TTTGATGATTCGTTTATGCGTCCGCTGTTTGGCGGGCGGGGATTCGTTCCGTTTTCGCG 1898  
Qy 1858 GGTTCCTCAAACCTGAGAGAAACCCCT 1881  
Db 1899 GGCCTCACAGTTGAGCAGAGCCCT 1922  
RESULT 4  
US-09-830-123-18  
; Sequence 18, Application US/09830123  
; Patent No. 6803500  
; GENERAL INFORMATION:  
; APPLICANT: Iida, Shigeru  
; APPLICANT: Tanaka, Sachiko  
; APPLICANT: Inagaki, Yoshishige  
; TITLE OF INVENTION: Genes Encoding Proteins Regulating the pH of Vacuoles  
; FILE REFERENCE: 001560-397  
; CURRENT APPLICATION NUMBER: US/09/830,123  
; CURRENT FILING DATE: 2001-04-24  
; PRIOR APPLICATION NUMBER: PCT/JP00/05722  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: JP 11/236800  
; PRIOR FILING DATE: 1999-08-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 2361  
; TYPE: DNA  
; ORGANISM: Torenia hybrida  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(2361)  
; OTHER INFORMATION: Nucleotide sequence of DNA encoding for protein regulating the pH of vacuoles  
; OTHER INFORMATION: pH of vacuoles  
US-09-830-123-18  
Query Match 34.6%; Score 754.4; DB 4; Length 2361;  
Best Local Similarity 69.4%; Pred. No. 2.2e-182;  
Matches 1090; Conservative 0; Mismatches 471; Indels 33; Gaps 2;  
Qy 319 TTATCGACATCTGATCAGCTCTCTGTGTTGCGTTGAATCTCTTTTGTGCACTTCTTTGT 378  
Db 444 TTGTGGAGCTCTGTGACGGTTCAGTGTGCTGCTATACCTTATTTGTGCTCTCTCTGC 503  
Qy 379 GCTTGTATGTTCTGTGTCATCTTTTGGAGAGATAGATGAGTGAACGAATCATCAACC 438  
Db 504 ACATGTATAGTATGTTGTCATCTTCGAGAGAAACCGTTGGATGAATCATCATTT 563  
Qy 439 GCCTTGTGATTCGGCTAGGCACCTGGTGTACCATTTTGTGTTAGTAAAGGAAAAGC 498  
Db 564 GCCCTCAATATGTTTAGCCACGGGAGTTATAATCTCTGTTAATAGTGGTGGAAAAGC 623  
Qy 499 TCGCATCTCTCTGCTTTTAGTGAAGATCTTTTCTTCATATATCTTTTGCACCATTTATA 558  
Db 624 TCCATCTCTGTGTTTTCAGTGAGGATCTTTCTTCATCTATGCGCTGCCACCAATCAT 683  
Qy 559 TTCAATCGAGGTTTCAAGTAAAGAGAGAGGTTTTCGCAATTTTCGTCATTTATG 618  
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Qy 619 CTTTTCGTCGCTGTGGAGCTATTATTTCTTGACATCATATCTCTAGGTGTAACACAG 678  
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Qy 679 TTCTTTAAGAGTTTGGACATTTGGAACCTTTGACTTTGGGTGAATTTATCTTATTTGGTGC 738  
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Qy 799 TTGCTTTACAGTCTTTGATTTCCGAGAGGGTGTGTGAATGATGCAACGTCAGTTTGTGTC 858

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Db 1101 CTATGTCATACATCATAAAAAGCTTATTTTGAAGCACTCACTGATCGGAGTT 1160  
QY 1039 GGCCTTATGATCTTATGCGGTATCTTCTATATGCTGTGAGCTTTTCGACTTGAAGC 1098  
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QY 1099 GGTATCTCACTGTGTTTCTGTTGTTATGTTGATGTCCTCAATACACATGCGCAATGTA 1158  
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QY 1159 ACGGAGAGCTCAAGATTAACAACAAGCATACCTTTGCAACTTTGTCATTTCTTCCGAG 1218  
Db 1281 ACTGAAACTCAAGAGTTACCAACAAGCATACATTTGCGACATTTGTCATTTGTCGAA 1340  
QY 1219 ACATTTATTTCTGTATGTTGGAATGGATGCTTTGGACATTTGCAAGTGAGATCCGTG 1278  
Db 1341 ATATTTATTTCTGTATGTTGGCATGGATGCTTTAGACATTTGAAATGAGATTCGTA 1400  
QY 1279 AGTGACACACCGGGAACTCGATCGCAGTGAGCTCAATCCTAATGGGTCTGTCATGTT 1338  
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QY 1339 GGAAGAGAGCGTTGCTCTTCGTTATCGTTTCTATCTAATCTTAGCAAGAGATCAA 1398  
Db 1461 TCAGAGAGCGCTTTGTTATTCCTTTATCATTTCTCTCAATCTGCGCAAAAGTCCCA 1520  
QY 1399 AGCGAGAAATCACTTTAAACATGAGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1458  
Db 1521 CTCGAAATTAATCAGTCTAGGAGCAAAATTAATATGTTGGTGGCTGTTGTTGTTGTTG 1580  
QY 1459 GCTGTATCTATGGCTCTTGATACAAAGTTTACAAGGGCGGGCAACAGATGATGCG 1518  
Db 1581 GCGGTTTCAATGGCTCTTGATCAAGAGTTTACTAGAGAGGTTCTCACAGTGAACGT 1640  
QY 1519 GGAATATGCAATCATGATACGAGTACGATTAATGTTGTTTATGACAGTGTGTTT 1578  
Db 1641 GAAATGCAATCATCACAGTACAAATCACCATTGTTGCTCTTCAGCACTGTGTTGTT 1700  
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Db 1701 GGTATGATGACCAAGCCCTCATCAATTTACTGATACCCCTACCAAGGCTTAACAGATCG 1760  
QY 1639 ATGTTATCTGATGACAAACCCCAAAATCCATACATATCCCTTTGTTGGACCAAGACTCG 1698  
Db 1761 GTCTCTTGAAACCGCTGACTCCAACTCCATCAATCCCACTTCTCGGGGAAAGTCAAG 1820  
QY 1699 TTTATGAGCCCTTC-----AGGGAACCACAATGTG 1728  
Db 1821 GACTCTGTGGCGCACTATTCAGATCAGAGGTCAAACTTCACAGGTGGCGAAGCCGTT 1880  
QY 1729 CTTGGCCTGACGATATAGTGGCTTCTTGACACGGCCCACTCGAACCGTGAATTAATAC 1788  
Db 1881 GCTCAACCGAGAGCCCTACGATGTTACTTCACAAAAGCCCACTCATACGGTGCATTAAT 1940  
QY 1789 TGGAGCAATTTGATGACTCTTTCATGCGACCGCTTTTGGAGGTCGTGGCTTTGTACCC 1848  
Db 1941 TGGAGAAATTCGACAAATGCTTTTATGCTCGGCTTTTGGTGGGGTGGCTTTGTACCA 2000  
QY 1849 TTTGTTCCAGGTTCTCCAACTGAGAGAAACCCCTC 1882

Db 2001 TATGTTCCGGTTCACCGACTGAACGAAGCGTTC 2034

RESULT 5

US-09-800-729-22  
; Sequence 22, Application US/09800729  
; Patent No. 6605592  
; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: 32 Human secreted proteins  
; FILE REFERENCE: P2044P1  
; CURRENT APPLICATION NUMBER: US/09/800,729  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: PCT/US00/26013  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 60/155,709  
; PRIOR FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 1581  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (112)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (959)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (1565)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-800-729-22

Query Match 4.2%; Score 91.2; DB 4; Length 1581;  
Best Local Similarity 47.6%; Pred. No. 3.8e-13;  
Matches 369; Conservative 6; Mismatches 370; Indels 30; Gaps 3;

QY 522 AGATCTTTCTTCATATATCTTTTCCACCCCATATATTTCAATTCAGAGGTTTCAAGTAAA 581  
Db 433 AGAAGTATTTTTCACATCTCTGCTCCCAATATTTTTCATGCTGATACAGCTTAAA 492  
QY 582 AAAGAAGCAGTTTTTCCGCAATTTTCGAGCTATTTATGCTTTTGGTGTGTTGGAGCTAT 641  
Db 493 GAAGAGACATTTTTCAGAAATCTTGGATCTATCTATGCTGCTATGCTTTCTTGGGACTGC 552  
QY 642 TATTTCTTGCAATCATATCTCTAGGTGTAAACAGAGTCTTTTAAAGAAAGTTGGAATT-- 699  
Db 553 TGTCTCATGCTTCATTTATTTGGAATCTCATGTATGTTGTTGTTGTTGTTGTTGTTGTTG 612  
QY 700 -----GGAACCTTTGACTTGGGTGATTTCTGCTATTTGTTGTTGTTGTTGTTGTTG 746  
Db 613 GGGACAGCTCTCAGATAAATTTTACTACAGAWTGTCTCTTTTGGAGCAATCATCTC 672  
QY 747 TGCAACAGATTTCAGTATGTACACTGCGAGTTCTGAATCAAGACGAGACACCTTTG---CT 803  
Db 673 TGCCACTGACCGAGTGTGCTGGCGATATTTAAATGAATTTGATGATGATGATGATGATG 732  
QY 804 TTACAGTCTTGTATTTGCGAGAGGTTGTTGTAATGATGCAACGTCAGTTGTTGTTGTTCAA 863  
Db 733 TTACGCACTTCTTTTGGAGAGAGCGTCTAAATGATGCTGTTGCTGTTGCTGTTGCTGCTC 792  
QY 864 CGCATTCAGAGCTTTGATCTCACTCACTCAACCAAGAGCTGCTTTTCTCTCTCTTGG 923  
Db 793 GTCTATTTGCTTACCAGCCGCGGAGTGAACACTCACGCTTTGATGCTGCTGCTT 852  
QY 924 AAATCTTGTATTTGTTCTTCCTAAGTACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 983  
Db 853 TTTTAAGTCAGTTGGCATTTTCTAGGTATATTTAGTGGCTCTTTTACCATGGGAGCTGT 912  
QY 984 TGGGTATGTTA-----TCAGAAAGCTATCTTTTGGAAAGGCACTCAACTGACCG 1031

Ds 913 GACTGGTGTGTGACTGCTCYAGTGACTAAGTTTATACCAACKGCACNGCTTCCCCCTGCT 972  
Qy 1032 AGAGTTGGCCCTTATGATGCTTATGGCGTAICCTTTCTTATATAGCTTGCTGAGCTTTTCGA 1091  
Ds 973 GGAGACGGCGCTGTTCTTCTCATGCTCTGGAGCAGCTTCTTCTTGGCAGAAGCCTGCGG 1032  
Qy 1092 CTTGAGCGGTATCCCTCACTGCTGTTTCTGTGGTATTGTGATGTCCTCCATTACACATGGCA 1151  
Ds 1033 ATTTACAGGTGTGTAGCTGCTCTTCTGTGGAATCAACAAGCTCATTACACCTACAA 1092  
Qy 1152 CAATGTAAACGGAGCTCAAGAATAACAACAAGCATACCTTTTGCAACTTTGTCAATTTCT 1211  
Ds 1093 CAATCTGCGTGGGAATCAAGAAGTCGAACCAAGCAGCTCTTTGAGGTGTTACATTTCT 1152  
Qy 1212 TCGGAGACATTTATTTCTTGTATGTTGGAAATGGATGCTTGGACATGACAAG 1266  
Ds 1153 GCGAGAGAACTTCATCTTCTCATATGGCGCTGGCACTGTTTACCTTCCAGAAG 1207

## RESULT 6

US-09-800-729-58

; Sequence 58, Application US/09800729

; Patent No. 6605592

; GENERAL INFORMATION:

; APPLICANT: Ni et al.

; TITLE OF INVENTION: 32 Human secreted proteins

; FILE REFERENCE: P2044P1

; CURRENT APPLICATION NUMBER: US/09/800,729

; CURRENT FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: PCT/US00/26013

; PRIOR FILING DATE: 2000-09-22

; PRIOR APPLICATION NUMBER: 60/155,709

; PRIOR FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 217

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 58

; LENGTH: 1354

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-800-729-58

Query Match 3.0%; Score 64.4; DB 4; Length 1354;

Best Local Similarity 54.7%; Pred. No. 2.5e-06;

Matches 128; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

Qy 1033 GAGTTGGCCCTTATGATGCTTATGGCGTATCTTCTTATATGCTTGCTGAGCTTTTCGAC 1092

Ds 18 GAGACGGCGCTGTTCTTCTCATGCTCTGGAGCAGCTTCTTGGCAGAAGCCTGCGGA 77

Qy 1093 TTGAGCGGTATCCCTCACTGCTGTTTCTGTGGTATTGTGATGTCCTCCATTACACATGGCA 1152

Ds 78 TTTACAGGTGTGTAGCTGCTCTTCTGTGGAATCACACAAGCTCATTACACCTACAA 137

Qy 1153 AATGTAACGGAGAGCTCAAGAATAACAACAAGCATACCTTTTGCAACTTTGTCAATTTCTT 1212

Ds 138 AATCTGTCGGTGGAAATCAAGAAGTCGAACCAAGCAGCTCTTTGAGGTGTTACATTTCTG 197

Qy 1213 GCGGAGACATTTATTTCTTGTATGTTGGAATGGATGCTTGGACATGACAAG 1266

Ds 198 GCGAGAGAACTTCATCTTCTCATATGGCGCTGGCACTGTTTACCTTCCAGAAG 251

## RESULT 7

US-09-800-729-57

; Sequence 57, Application US/09800729

; Patent No. 6605592

; GENERAL INFORMATION:

; APPLICANT: Ni et al.

; TITLE OF INVENTION: 32 Human secreted proteins

; FILE REFERENCE: P2044P1

; CURRENT APPLICATION NUMBER: US/09/800,729

; CURRENT FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: PCT/US00/26013

; PRIOR FILING DATE: 2000-09-22

; PRIOR APPLICATION NUMBER: 60/155,709

; PRIOR FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 217

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 57

; LENGTH: 1688

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (21)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: SITE

; LOCATION: (69)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: SITE

; LOCATION: (99)

; OTHER INFORMATION: n equals a,t,g, or c

US-09-800-729-57

Query Match 3.0%; Score 64.4; DB 4; Length 1688;

Best Local Similarity 54.7%; Pred. No. 2.7e-06;

Matches 128; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

Qy 1033 GAGTTGGCCCTTATGATGCTTATGGCGTATCTTCTTATATGCTTGCTGAGCTTTTCGAC 1092

Ds 345 GAGACGGCGCTGTTCTTCTCATGCTCTGGAGCAGCTTCTTGGCAGAAGCCTGCGGA 404

Qy 1093 TTGAGCGGTATCCCTCACTGCTGTTTCTGTGGTATTGTGATGTCCTCCATTACACATGGCA 1152

Ds 405 TTTACAGGTGTGTAGCTGCTTCTTCTGTGGAATCACACAAGCTCATTACACTACAAC 464

Qy 1153 AATGTAACGGAGAGCTCAAGAATAACAACAAGCATACCTTTTGCAACTTTGTCAATTTCTT 1212

Ds 465 AATCTGTCGGTGGAAATCAAGAAGTCGAACCAAGCAGCTCTTTGAGGTGTTACATTTCTG 524

Qy 1213 GCGGAGACATTTATTTCTTGTATGTTGGAATGGATGCTTGGACATGACAAG 1266

Ds 525 GCGAGAGAACTTCATCTTCTCATATGGCGCTGGCACTGTTTACCTTCCAGAAG 578

## RESULT 8

US-09-949-016-849

; Sequence 849, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: C0001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 849

; LENGTH: 4452

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-849

Query Match 2.8%; Score 60.6; DB 4; Length 4452;

Best Local Similarity 47.7%; Pred. No. 3.8e-05;

Matches 365; Conservative 0; Mismatches 364; Indels 36; Gaps 5;

Qy 514 TTTAGTGAAGATCTTTTCTTTCATATATCTTTTGGCACCCTATATATTCAATGCAAGGTTT 573





Db 173 CCCTCTCTTGAAGAACTGAACATAAATGTGATTAATGAGCGCACATTATTTATATTT 114  
QY 2074 GTAATTATATTCATATTTGTTTGTGTAACACAACTACACATTTGTTTATGTTTGA 2133  
Db 113 GATATATACCACTTTGTATCATATTTGCTTTTATTTTTCATTTTATTTTCA 54  
QY 2134 TTTGGTTTTCGTAACAAAAAATTTTATTTTATTTTATTTTATTTTATTTTCA 2178  
Db 53 AATATATGTTTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTCA 9

## RESULT 13

US-09-005-051-36

; Sequence 36, Application US/09005051

; Patent No. 6291222

; GENERAL INFORMATION:

; APPLICANT: Silver, Gary W.

; APPLICANT: Wisniewski, Nancy

; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; ADDRESSEE: Heska Corporation

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/005,051

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/747,221

; FILING DATE: No. 6291222ember 12, 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Verser, Carol Talkington

; REGISTRATION NUMBER: 37,459

; REFERENCE/DOCKET NUMBER: FC-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 970/493-7272

; TELEFAX: 970/484-9505

; INFORMATION FOR SEQ ID NO: 36:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2007 nucleotides

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 11..1594

US-09-005-051-36

Query Match 2.5%; Score 53.8; DB 3; Length 2007;  
Best Local Similarity 52.4%; Pred. No. 0.0015;  
Matches 118; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 1954 AAATATGCTTTTGTGTAATAATTCATTTGTAATATTTGTTGTGAGACAGAAATCTGT 2013  
Db 1775 AACAAATCTGTTTGTAGTATTTGCGCATTTCAACAGATGGTGTACTGTGCTAAATTTGT 1834  
QY 2014 CCTAACGTTTGTGAGACAGAAAGCAACATGCGCACTTTTGAAGTGTGTTGATGATGAT 2073  
Db 1835 CGCTCTTCTTGAAGAACTGAACATAAAATGTAATTAATGAGCGCACATTATTTATATTT 1894  
QY 2074 GTAATTATATTCATATTTGTTTGTGTAACACAACTACACATTTGTTTATGTTTGA 2133

Db 1895 GATATTATACCACTTTGTATCATATTTGCTTTTATTTTTCATTTTATTTTCA 1954  
QY 2134 TTTGGTTTTCGTAACAAAAAATTTTATTTTATTTTATTTTATTTTATTTTCA 2178  
Db 1955 AATATATGTTTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTCA 1999

## RESULT 14

US-09-005-051-38/c

; Sequence 38, Application US/09005051

; Patent No. 6291222

; GENERAL INFORMATION:

; APPLICANT: Silver, Gary W.

; APPLICANT: Wisniewski, Nancy

; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; ADDRESSEE: Heska Corporation

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/005,051

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/747,221

; FILING DATE: No. 6291222ember 12, 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Verser, Carol Talkington

; REGISTRATION NUMBER: 37,459

; REFERENCE/DOCKET NUMBER: FC-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 970/493-7272

; TELEFAX: 970/484-9505

; INFORMATION FOR SEQ ID NO: 38:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2007 nucleotides

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-09-005-051-38

Query Match 2.5%; Score 53.8; DB 3; Length 2007;  
Best Local Similarity 52.4%; Pred. No. 0.0015;  
Matches 118; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 1954 AAATATGCTTTTGTGTAATAATTCATTTGTAATATTTGTTGTGAGACAGAAATCTGT 2013  
Db 233 AACAAATCTGTTTGTAGTATTTGCGCATTTCAACAGATGGTGTACTGTGCTAAATTTGT 174  
QY 2014 CCTAACGTTTGTGAGACAGAAAGCAACATGCGCACTTTTGAAGTGTGTTGATGATGAT 2073  
Db 173 CGCTCTTCTTGAAGAACTGAACATAAAATGTAATTAATGAGCGCACATTATTTATATTT 114  
QY 2074 GTAATTATATTCATATTTGTTTGTGTAACACAACTACACATTTGTTTATGTTTGA 2133  
Db 113 GATATTATACCACTTTGTATCATATTTGCTTTTATTTTTCATTTTATTTTCA 54  
QY 2134 TTTGGTTTTCGTAACAAAAAATTTTATTTTATTTTATTTTATTTTATTTTCA 2178  
Db 53 AATATATGTTTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTCA 9



